

Targeting Receptor Tyrosine Kinase Signaling in Acute Myeloid Leukemia

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ABBREVIATIONS

AML	Acute Myeloid Leukemia
Ara-C	Cytarabine
ATRA	All- <i>Trans</i> -Retinoic Acid
AT/RT	Atypical Teratoid/Rhabdoid Tumor
CBF	Core Binding Factor
CBF-AML	Core Binding Factor Leukemia
CBP	Creb-Binding Protein
CML	Chronic Myeloid Leukemia
CNS	Central Nervous System
CSF-I	Colony-Stimulating Growth Factor I
4E-BP	4E-Binding Protein
EGF	Epidermal Growth Factor
ERK	Extracellular Signal-Regulated Kinase
FAB	French-American-British Classification
FGF	Fibroblast Growth Factor
FKHR	Forkhead
FLT3	Fms-like Tyrosine Kinase 3
FL	FLT3 Ligand
FTI	Farnesyltransferase Inhibitor
GBM	Glioblastoma Multiforme
GPCR	G-Protein Coupled Receptor
GSK-3	Glycogen Synthase Kinase-3
IGF	Insulin-like Growth Factor
IGFBP1-6	Insulin-like Growth Factor Binding Protein 1-6
IGF-IR	Insulin-like Growth Factor I Receptor
IR	Insulin Receptor
IRS	Insulin Receptor Substrates
ITD	Internal Tandem Duplication
JAK	Janus Protein Tyrosine Kinase
M-6-PR	Mannose 6-Phosphate Receptor; IGF-II Receptor
MB	Medulloblastoma
MDM-2	Murine Double Minute Gene 2

MDS	Myelodysplastic Syndrome
MM	Multiple Myeloma
MPD	Myeloproliferative Disease
MRT	Malignant Rhabdoid Tumor
mTOR	Mammalian Target of Rapamycin
NB	Neuroblastoma
PDGF	Platelet-Derived Growth Factor
PDK1	Phosphoinositide-dependent Kinase-1
PI	Phosphatidylinositol
PI3K	Phosphoinositide 3-Kinase
PI(3)P	Phosphatidylinositol-3-Monophosphate
PI(3,4)P ₂	Phosphatidylinositol-3,4-Bisphosphate
PI(3,4,5)P ₃ ; PIP ₃	Phosphatidylinositol-3,4,5-Trisphosphate
PKB	Protein Kinase B (also termed Akt)
PTK	Protein Tyrosine Kinase
RA	Rheumatoid Arthritis
RAR α	Retinoic Acid Receptor Alpha
Rheb	Ras Homologue Enriched in the Brain
RNAi	RNA Interference
RTK	Receptor Tyrosine Kinase
S6K	Ribosomal Protein S6 Kinase
SCLC	Small Cell Lung Cancer
Shc	Src-Homology Collagen Protein
shRNA	Small Hairpin RNA
SOS	Son of Sevenless
STAT	Signal Transducer and Activator of Transcription
TSC1, TSC2	Tuberous Sclerosis Complex 1 and 2

1. A. SUMMARY

The acute myeloid leukemia (AML) is a quickly progressing, heterogeneous clonal disorder of hematopoietic progenitor cells. A significant progress in the understanding the pathogenesis of AML has been achieved in the past few years. Two major types of genetic events are thought to give rise to leukemic transformation: alterations in the activity of transcription factors controlling hematopoietic differentiation and activation of components of receptor tyrosine kinase (RTK) signaling pathways. This has led to the development of promising new therapeutic strategies for the disease. Recent developments in the field of molecularly targeted therapies for AML involve RTKs such as the FMS-like tyrosine kinase 3 (Flt3), c-Kit and signal transduction via the phosphoinositide 3-kinase (PI3K) and mitogen-activated protein kinase (MAPK) pathways. Initial results imply that targeting RTKs is a very promising approach for AML and that other receptors, such as the insulin-like growth factor receptor (IGF-IR), could also represent new targets in the future.

The main goal of this work was therefore aimed at gaining deeper insight into RTK signaling in a panel of AML cell lines and patient blast cells. A broad protein expression analysis was set up in order to identify cancer-specific expression patterns of signaling molecules and to uncover potential molecular targets. Using different approaches the molecular function and the feasibility of targeting the candidate proteins was investigated. Novel specific inhibitors were tested and neutralizing antibodies and RNA interference (RNAi) were used to block or down-regulate the individual proteins. Our study of the IGF-IR/PI3K signaling system in AML cells uncovered a novel role for autocrine IGF-I signaling in the growth and survival of these cancer cells. Besides, we could show that targeting this signaling branch in combination with commonly used chemotherapeutical agents represents an interesting novel approach for AML therapy.

As protein expression analysis revealed highly variable expression levels of the mammalian target of rapamycin (mTOR) in the panel of cells analyzed, further interest was laid on the role of mTOR in AML. Cells expressing low levels of mTOR were compared to cells expressing high levels of this protein and a siRNA screen was aimed at uncovering human kinases that modulate the sensitivity to the mTOR inhibitor rapamycin. Preliminary results suggest that mTOR plays a crucial role in cell growth and survival in a subset of AML cells and that rapamycin in combination with certain RTK or Syk/ZAP70 inhibitors has potential for AML therapy.

Another study investigating RTK signaling in childhood central nervous system (CNS) tumors revealed autocrine insulin production by the cancer cells and a crucial role of this growth factor and the insulin receptor (IR)/PI3K signaling pathway for cellular growth and survival of the malignant cells.

Moreover, our interest was set on elucidating the specific role of individual PI3K isoforms in human cancer. The PI3Ks are a family of lipid kinases which transduce signals from RTKs and play a crucial role in a variety of intracellular signaling events including the control of cell growth and survival. Nevertheless, the specific functions of the individual isoforms in human cancer has not been completely understood yet. In view of the search for specific molecular targets for cancer therapy, an extensive knowledge of the exact role and function of these signaling enzymes is of high importance. Therefore, PI3K isoforms were specifically targeted in human cancer cells and the effect on cellular responses was investigated. In AML, a predominant role of the class I_A PI3Ks p110 β and p110 δ for cell growth, survival and chemo-resistance could be described. In an extensive study of PI3K isoforms in human neuroblastoma, a novel function of p110 δ in growth and survival of this type of cancer could be identified. Since much less attention has been paid to the role of the class II PI3Ks in human cancer, our work was aimed at elucidating the expression pattern and function of PI3KC2 β in a panel of human tumor cells including AML, different brain tumors and neuroendocrine tumors. Novel isoform-specific inhibitors were tested and with the use of RNAi it could be shown that PI3KC2 β contributes to cell survival, proliferation and migration of various human cancer cells.

In summary, our study of the RTK/PI3K signaling system in distinct human cancers has provided novel insights into the importance and the complexity of this network for tumor growth and survival. Moreover, the analysis of specific components of this crucial signaling network has uncovered potential molecular targets for future cancer therapy.

1. B. ZUSAMMENFASSUNG

Die akute myeloide Leukämie (AML) ist eine bösartige monoklonale Krankheit der hämatopoitischen Vorläuferzellen mit einem rasch progredienten klinischen Verlauf. Hinsichtlich der Ätiopathogenese konnten aber in den letzten Jahren wichtige neue Erkenntnisse gewonnen werden, so dass man heute v.a. von zwei essentiellen genetischen Veränderungen ausgeht, die hauptsächlich zur Entstehung dieser Krebsart beitragen: 1) Veränderungen in der Aktivität von Transkriptionsfaktoren, welche die Differenzierung der hämatopoitischen Zellen kontrollieren, sowie 2) die Aktivierung von Komponenten des Rezeptor-Tyrosinkinase (RTK)-Signalweges. Diese Faktoren stellen eine wichtige Grundlage für die Entwicklung neuartiger Strategien in der Krebstherapie dar. Aktuelle Errungenschaften im Gebiet der zielgerichteten AML-Therapien fokussieren bereits auf RTKs. Zudem gibt es Studien, welche zum Beispiel die FMS-like tyrosine kinase 3 (FLT3), c-Kit oder die Signalübermittlung via phosphoinositide 3-kinase (PI3K) und die mitogen-activated protein Kinase (MAPK) als molekulares Ziel beschreiben. Erste Resultate zeigen auch, dass die RTKs als therapeutisches Ziel eine sehr erfolgversprechende Strategie darstellen. Eine Vielzahl weiterer Kandidaten aus dieser Gruppe - wie zum Beispiel der insulin-like growth factor receptor (IGF-IR) - wird gegenwärtig in vitro sowie in präklinischen Studien untersucht.

Der Hauptfokus meiner Doktorarbeit lag daher im detaillierten Studium der Signalübermittlung durch RTKs in verschiedenen AML-Zelllinien und Vorläuferzellen (Blasten) von AML-Patienten. Eine ausführliche Analyse galt dabei der Expression von verschiedenen Proteinen, welche eine Rolle in der intrazellulären Signalübertragung spielen, um so ein spezifisches Musters für Krebszellen zu identifizieren. Mit Hilfe von verschiedenen Techniken wurde dann die genaue molekulare Funktion der Kandidaten untersucht und ihr Potential als therapeutisches Ziel analysiert. Schliesslich wurden neue, spezifische Inhibitoren getestet und neutralisierende Antikörper und RNA-Interferenz (RNAi) zur zielgerichteten Hemmung der gewünschten Proteine angewendet.

Eine umfangreiche Analyse des IGF-IR/PI3K Netzwerkes in AML-Zellen zeigte insbesondere, dass die leukämischen Zellen in der Lage sind, IGF-I selber zu produzieren und zu sezernieren. Damit konnte eine neue, autokrine Rolle von IGF-I für das Wachstum und Überleben der Krebszellen beschrieben werden. Zugleich konnten wir zeigen, dass dieses System ein

vielversprechender molekularer Angriffspunkt in der Krebstherapie ausmacht, v.a. in Kombination mit klinisch bereits eingesetzten Chemotherapeutika.

Daneben zeigte die Analyse der Proteinexpression in AML-Zellen eine ausgeprägte Variabilität des mammalian target of rapamycin (mTOR). In einem nächsten Schritt haben wir deshalb die funktionelle Rolle von mTOR in AML weiter untersucht. Dabei wurden Zelltypen mit einer starken Expression von mTOR gegenüber einer geringen mTOR-Expression verglichen. Mittels eines siRNA-screens suchten wir zudem nach Kinasen, welche die Sensitivität zum mTOR Inhibitor Rapamycin beeinflussen. Erste Resultate zeigten, dass mTOR eine wichtige Rolle für das Wachstum und Überleben in einer Gruppe von AML Zellen spielt und dass Rapamycin in Kombination mit gewissen RTK oder SYK/ZAP70 Inhibitoren als mögliche neue Therapeutika der AML in Frage kommen.

In einer anderen Studie konnten wir zeigen, dass in pädiatrischen Tumoren des Zentralnervensystems (ZNS) die autokrine Produktion von Insulin eine essentielle Rolle für das Wachstum und Überleben der Krebszellen spielt.

Des Weiteren wurde die spezifische Funktion der verschiedenen PI3K Isoformen in Krebs untersucht. Die PI3Ks bilden eine Familie von Kinasen, welche als wichtige Mediatoren von intrazellulären Signalen eine Vielfalt von zellbiologischen Vorgängen kontrollieren, in erster Linie aber Wachstum und Überleben der Zelle. Dennoch fehlen bis heute weitgehend Studien, welche die verschiedenen PI3K-Isoformen nach ihrer spezifischen Relevanz untersucht haben. Die Suche nach geeigneten molekularen Zielen für die Krebstherapie stellt jedoch unumgänglich eine fundierte Kenntnis der exakten Funktion von potentiellen Kandidaten dar. Daher haben wir spezifische PI3K-Isoformen untersucht und ihre Rolle in zellulären Antworten analysiert. In AML konnten so die PI3K-Isoformen p110 δ und p110 β als wichtigste Isoformen für Wachstum und Überleben der Krebszelle sowie deren Resistenz gegenüber Chemotherapeutika identifiziert werden. Diese Daten konnten zudem in einer Analyse von PI3K-Isoformen in Neuroblastomen bestätigt werden. Da der Rolle von PI3Ks der Klasse II in Krebszellen bis heute noch kaum Beachtung geschenkt wurde, haben wir eine umfangreiche Studie zur Expression und Funktion von PI3KC2 β in verschiedenen Krebsarten (AML, Hirntumoren und neuroendokrine Tumoren) durchgeführt. Es wurden neue Isoform-spezifische Inhibitoren getestet und mittels RNAi konnte

gezeigt werden, dass PI3KC2 β zum Überleben und Wachstum, wie auch zur Migration von Krebszellen beiträgt.

Zusammengefasst gibt die vorliegende Dissertation bedeutende Einblicke in die Komplexität des RTK/PI3K Netzwerkes und unterstreicht die Wichtigkeit dieses Signalsystemes für das Wachstum und Überleben von Krebszellen. Zudem konnten durch die fundierte Untersuchung von einzelnen Komponenten dieses Systemes neue potentielle Ziele zur Krebstherapie identifiziert werden.

2. INTRODUCTION

2.1. Acute Myeloid Leukemia

Acute leukemias represent a small (<3%) fraction of all human cancers, but are a leading cause of cancer-related mortality in children and young adults (Deschler & Lubbert, 2006; Kolitz, 2006). The acute myeloid leukemia (AML) accounts for about 25% of all leukemias in adults in the Western world, and is the second most frequent form of leukemia following chronic lymphocytic leukemia (CLL) (Deschler & Lubbert, 2006). The incidence of AML is 3.4 cases per 100,000 general population. AML is a heterogeneous group of diseases characterized by uncontrolled clonal proliferation of hematopoietic precursor cells leading to impairment of normal hematopoietic cell production, causing cytopenias. Based on the cell type of which the leukemia cell developed together with the degree of its maturity, the French-American-British (FAB) classification system groups AML into eight subtypes, M0 through M7 (Table 1). The different subtypes are known to have varying clinical prognoses and therapy responses.

French-American-British Classification (FAB)	
M0	<i>undifferentiated AML</i> the bone marrow cells show no significant signs of differentiation
M1	<i>myeloblastic leukemia, without differentiation</i> the bone marrow cells show minimal signs of maturation (granulocyte differentiation)
M2	<i>myeloblastic leukemia, with differentiation</i> the bone marrow cells are at or beyond the promyelocyte stage (early granulocyte)
M3	<i>promyelocytic leukemia</i> most cells are abnormal early granulocytes between the stage of myeloblasts and myelocytes
M4	<i>myelomonocytic leukemia</i> variable amounts of differentiated granulocytes and monocytes in the bone marrow and circulating blood; > 20% monocytes and promonocytes in the bone marrow
M5	<i>monoblastic or monocytic leukemia</i> poorly differentiated monoblasts (immature monocytes) with lacy-appearing genetic material or large population of monoblasts, promonocytes, and monocytes
M6	<i>erythroleukemia</i> abnormal red blood cell-forming cells making up over half of the nucleated cells in the bone marrow
M7	<i>megakaryoblastic leukemia</i> immature megakaryocytes or lymphoblasts

Table 1: French-American-British Classification of AML

The World Health Organization Classification (WHO) subdivides the AMLs into 4 major categories: AML with recurrent cytogenetic translocations; AML with multilineage dysplasia; AML and myelodysplastic syndromes (MDS), therapy-related; and AML not otherwise categorized (Table 2). This system provides prognostic information in terms of cytogenetic findings and associated myelodysplastic changes in the AML.

World Health Organization Classification (WHO)	
AML with recurrent cytogenetic translocations	t(8;21)(q22;q22) AML1/CBF α /ETO t(15;17)(q22;q12) and variants PML/RAR α inv(16)(p13;q22) t(16;16)(p13;q22) CBF β /MYH1 11q23 MLL abnormalities Patients generally have a high rate of remission and a better prognosis compared to other types of AML.
AML with multilineage dysplasia	Myelodysplastic syndrome (MDS) or myeloproliferative disease (MPD) that transformed into AML. Occurs often in elderly patients and often with a worse prognosis.
AML and MDS, therapy-related	AML or MDS developed after chemotherapy and/or radiation therapy. Often characterized by specific chromosomal abnormalities and often with a worse prognosis.
AML not otherwise categorized	AML subtypes that do not fall into the above categories.

Table 2: World Health Organization Classification of AML

During the past decade, there has been a shift in AML diagnosis, classification, and treatment strategies from protocols relying on cell morphology and cytochemistry, to cell-surface antigen expression and the use of cytogenetic and molecular markers. Treatment of AML, however, still represents a difficult challenge because of relapse and complications associated with treatment (Kolitz, 2006). In the past 40 years, advances in supportive care and development of chemotherapeutic agents have led to improved outcomes in patients with acute myeloid leukemia. High relapse rates following remission have led to extensive efforts to develop techniques and regimens for detecting and eliminating minimal residual disease. Since standard cytotoxic chemotherapies have side effects to which AML patients, especially those of advanced age, are susceptible, there is a need to develop new therapies to overcome these difficulties (Deschler & Lubbert, 2006; Estey & Dohner, 2006). A better understanding of the biology and the molecular pathogenesis of AML has led to the development of new, targeted agents and strategies for AML treatment. Targeted therapy has indeed improved outcomes in some AML patients. Most of the

new agents used for AML therapy are less toxic than their predecessors, and combinations with more intensive traditional regimens are being tested.

2.1.1. Pathogenesis

Great efforts have been made to gain a better understanding of the molecular pathogenesis of AML. The malignancy is characterized by an accumulation of granulocyte or monocyte precursors in the blood. This is caused by the clonal growth of immature progenitor cells, which display increased proliferation and resistance to apoptosis, as well as impaired differentiation (Steffen et al., 2005).

Recurring chromosomal translocations are a hallmark of human leukemias. There are more than 300 recurring chromosomal translocations, of which more than 100 have been cloned (Kelly & Gilliland, 2002), providing important insights into the pathogenesis of the disease. Chromosomal aberrations are found in about half of all AML cases and are grouped into two major subtypes: balanced and unbalanced aberrations (Hiddemann et al., 2005). The biology of AML with balanced chromosomal translocations is fairly well understood, in contrast to the situation in AML with unbalanced aberrations (Hiddemann et al., 2005). Moreover, nearly half of all AML cases present a non-aberrant karyotype (Frohling et al., 2005; Hiddemann et al., 2005). In this category of AML, molecular analyses have revealed mutations in the *FLT3*, *CEBPA*, *KIT* and *NPM* genes, as well as *MLL* partial tandem duplication (Frohling et al., 2005; Hiddemann et al., 2005).

In AML, chromosomal translocations often result in loss-of-function mutations in transcription factors that are required for normal hematopoietic development (Kelly & Gilliland, 2002; Steffen et al., 2005; Tenen, 2003). The elucidation of the structure and function of leukemogenic genes, as well as the analysis of their occurrence in leukemia has led to a two-hit model of AML pathogenesis. According to this model, AML develops as a result of the concurrent emergence of two classes of genetic alterations (mutations or gene rearrangements). While class I mutations confer a proliferative and/or survival advantage to hematopoietic progenitors (Kelly & Gilliland, 2002; Steffen et al., 2005), class II mutations lead to impaired hematopoietic differentiation. The increase in cell proliferation and survival of leukemic blasts (class I mutations) is thought to be caused by alterations in receptor tyrosine kinase (RTK) signaling pathways. In this context, it has been demonstrated that mutations in FMS-like tyrosine kinase 3 (Flt3), c-Kit and Ras are frequent in AML (Kelly & Gilliland, 2002; Steffen et al., 2005). The activation status of growth

and survival pathways including phosphoinositide 3-kinase (PI3K)/Akt has also been found to be increased in AML blasts (Martelli et al., 2006). The impaired differentiation of AML blasts (class II mutation) is thought to occur through alterations in transcription factors required for normal myeloid cell differentiation (Kelly & Gilliland, 2002; Steffen et al., 2005; Tenen, 2003). In AML, these transcription factors are frequently the target of translocations, leading to the expression of fusion proteins such as AML1/ETO, CBF β /SMMHC, PML-RAR α , or MLL fusion proteins (Kelly & Gilliland, 2002; Steffen et al., 2005).

2.1.2. Genetic Alterations Involving Transcription Factors

Transcription factors are frequently targeted by balanced chromosomal translocations in AML. These include core binding factor (CBF), retinoic acid receptor alpha (RAR α), and members of the HOX family of transcription factors (Kelly & Gilliland, 2002; Steffen et al., 2005; Tenen, 2003). Transcriptional coactivators, such as Creb-binding protein (CBP), p300, MOZ, TIF2, and MLL, are also targets of chromosomal translocations in AML (Kelly & Gilliland, 2002; Steffen et al., 2005). The targeted transcription factors are thought to be important for normal hematopoietic development. The consequence of the chromosomal translocations found in AML is loss-of-function and therefore impaired hematopoietic differentiation. For example, CBF is a heterodimeric transcription factor composed of a DNA-binding component, AML1, and the CBF β subunit which functions as a transcriptional activator of AML1. CBF controls the expression of genes that are critical for normal hematopoietic development. The three most common translocations involving CBF are the t[8;21], inv[16], and t[12;21] that result in expression of the AML1/ETO, CBF β /SMMHC, and TEL/AML1 fusion proteins, respectively. Each of these fusion proteins is a dominant negative inhibitor of CBF-mediated transcription. Transcriptional repression of CBF target genes by CBF-related fusion proteins is thought to be mediated through aberrant recruitment of the nuclear corepressor/histone deacetylase complex. Another example are fusion genes involving RAR α , such as PML/RAR α associated with the t[15;17] translocation in acute promyelocytic leukemia. Expression of the PML/RAR α fusion protein results in a block of differentiation at the promyelocyte stage caused in part by the recruitment of the nuclear corepressor complex. This block is relieved by all-*trans*-retinoic acid (ATRA), which induces the release of the nuclear corepressor complex by binding to PML/RAR α . In addition to these direct inhibitory effects on transcriptional activation, the fusion

proteins may also have additional roles in impairment of hematopoietic differentiation (Kelly & Gilliland, 2002).

Interestingly, in hematological clonal disorders in children with Down Syndrome (DS), mutations are commonly found in the gene encoding the transcription factor GATA-1 (Wechsler et al., 2002). The incidence of childhood acute leukemia is highly increased in children with DS, with a prevalence of acute megakaryoblastic leukemia (FAB M7) (Kurkjian et al., 2006). GATA-1 is known to be critical for normal development of erythroid and megakaryocytic lineages, and the absence of GATA-1 promotes the accumulation of immature megakaryocytes (Magalhaes et al., 2006). The fact that mutations in GATA-1 occur in nearly every case of DS with a myeloproliferative disorder suggests that deregulation of GATA-1 is an essential step in the development of the disease in this particular patient group (Gurbuxani et al., 2004). Even though a direct link between trisomy 21 and the X-linked transcription factor GATA-1 have not been found so far, models including gene dosage effects have been proposed and trisomy 21 is thought to cooperate with the non- or dysfunctional GATA-1 in the multistep process in which progenitor cells acquire multiple genetic lesions (Gurbuxani et al., 2004).

2.2. Receptor Tyrosine Kinase Signaling

Receptor tyrosine kinases (RTKs) are central components of cell signaling networks and play a crucial role in normal physiological processes such as in embryogenesis and development. RTK networks control fundamental cellular activities including cell proliferation and survival, cell cycle control, metabolism, as well as cell shape and movement. They are able to detect, filter, and process a variety of environmental and intercellular factors. Numerous membrane spanning surface receptors have been identified and classified based on ligand preference, the induction of biological responses and their primary structure. Protein tyrosine kinases (PTKs) are endowed with intrinsic protein kinase activity that catalyzes the transfer of γ -phosphate of ATP to tyrosine residues of protein substrates (Hubbard et al., 1998). The receptor tyrosine kinases (RTKs) are one large family of PTKs that contain an intracellular catalytic protein tyrosine kinase domain, an extracellular ligand binding domain and regulatory sequences. More than 50 mammalian RTKs are known so far including the well known insulin receptor (IR), Fms-like tyrosine kinase 3 (FLT3), c-Kit, epidermal growth factor (EGF), platelet derived growth factor (PDGF), fibroblast

growth factor (FGF), colony-stimulating growth factor I (CSF-I) and insulin-like growth factor I (IGF-I) receptor (Hunter, 1998). A plethora of ligands such as peptides, proteins, lipids, or carbohydrates bind to and regulate the pleiotropic actions of RTKs. Tight control of the receptor activity is maintained by protein-tyrosine phosphatases, by other serine/threonine kinases, as well as autoregulatory mechanisms in the receptors. The extracellular binding of a specific ligand to a RTK induces conformational alterations that are translated across the membrane barrier resulting in the activation of its intracellular kinase activity (Schlessinger, 1988). In general, ligand binding induces allosteric interactions causing dimerization of receptor subunits through disulfide-bridges (Riedel et al., 1989) and autophosphorylation of specific tyrosine residues within their cytoplasmatic domains (Jiang & Hunter, 1999; Schlessinger, 1988). Dimerization-mediated receptor activation mechanisms have been described for receptors composed of heterotetrameric structures such as the IR, IGF-IR, PDGFR and the EGFR. Tyrosine autophosphorylation stimulates the intrinsic kinase activity of the receptor and leads to the generation of recruitment sites for downstream signal transducers. Src homology-2 (SH2) (Schaffhausen, 1995) or phosphotyrosine-binding (PTB) (Zhou & Fesik, 1995) domains are known phosphotyrosine-recognition domains present in various signaling proteins.

Activation of RTKs leads to rapid stimulation of phosphatidylinositol metabolism and the generation of multiple second messengers. One well characterized signaling pathway downstream of the IR and IGF-IR involves the insulin receptor substrates-1 to -4 (IRS-1 to -4) and the Src-homology collagen protein (Shc) isoforms as adapter molecules. The adapter proteins bind to the phosphotyrosine residues within the juxtamembrane region of the cytoplasmatic receptor and undergo subsequent tyrosine phosphorylation. Phosphorylation of the IRS adapter molecules on one hand triggers activation of the phosphoinositide 3-kinase (PI3K)/Akt signaling pathway (Myers et al., 1993; Vanhaesebroeck et al., 1997a; Yamamoto et al., 1992), whereas, on the other hand, the Shc adapter activates signaling by the Ras/Raf/MAPK pathway (reviewed in (Vanhaesebroeck et al., 1997a)). Generally, signals transduced through those signaling cascades have pleiotropic effects on cell behavior controlling cell proliferation, differentiation and cell migration, as well as apoptosis (Peruzzi et al., 1999). The PI3Ks phosphorylate phosphatidylinositol (PI) on the D-3 position of the inositol ring, producing distinct second messengers such as PI(3)P, PI(3,4)P₂ and PI(3,4,5)P₃ (PIP₃) (Katso et al., 2001). These lipid products activate signal transduction by diverse proteins including phosphoinositide-dependent kinase-1 (PDK1), forkhead (FKHR), glycogen synthase kinase-3 (GSK-3), tuberous sclerosis

complex 1 and 2 (TSC1, TSC2), BAD, Ras homologue enriched in the brain (Rheb), mammalian target of rapamycin (mTOR), 4E-binding protein (4E-BP) and ribosomal protein S6 kinase (S6K) (Katso et al., 2001). The Ras/Raf/extracellular signal-regulated kinase (Erk) cascade proceeds from Ras and its downstream effector Raf to Erk (p42/44 MAPK) (Seger & Krebs, 1995).

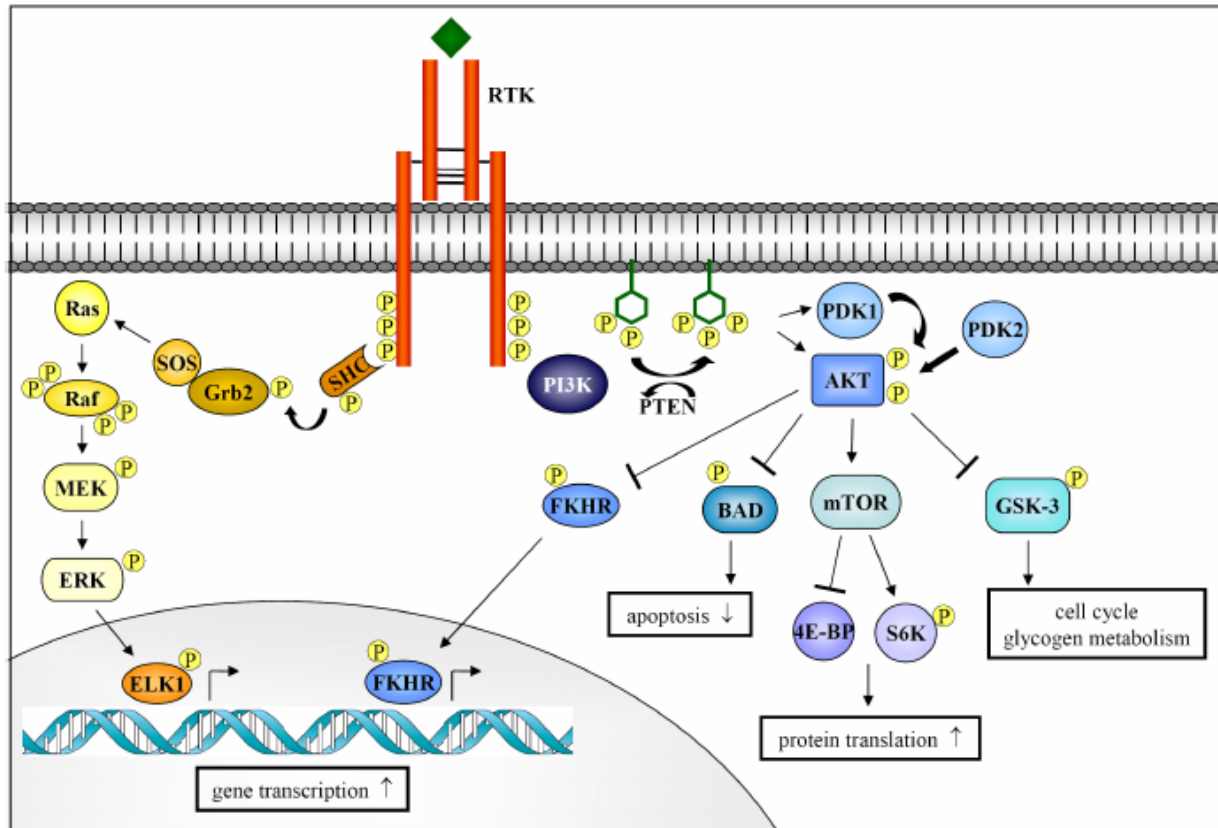


Fig. 1: Overview of RTK signaling. Signals are transduced via the mitogen-activated protein kinase (MAPK) or the phosphoinositide 3-kinase (PI3K) pathway. Key upstream regulators of MAPK signaling include growth factor receptor-bound protein 2 (Grb2), Son of Sevenless (SOS), Ras, Raf, MAPK/Erk kinase (MEK), extracellular signal-regulated kinase (ERK) and ELK1. Activation of the PI3K pathway is initiated by recruitment of the PI3K complex to the phosphorylated receptor. Downstream signals are transduced via phosphoinositide-dependent kinase 1 (PDK1), protein kinase B/Akt (AKT), the mammalian target of rapamycin (mTOR), 4E-binding protein (4E-BP) and ribosomal protein S6 kinase (S6K), forkhead (FKHR), BAD and glycogen synthase kinase-3 (GSK3).

Protein tyrosine phosphorylation was discovered more than 25 years ago (Hunter & Sefton, 1980) and protein tyrosine kinases, the signaling pathways they activate, as well as the mechanisms underlying their action and regulation have been widely studied. The importance of understanding the complexity of signaling networks, their regulation and the RTK interconnections has been highlighted by a large variety of molecular alterations and deregulations found in various human diseases including cancer.

2.2.1. Insulin-like Growth Factor I Receptor Signaling

The Insulin/IGF family of cell signaling factors comprises a phylogenetically conserved system with a critical role in growth and development of many tissues and the regulation of overall growth and metabolism. A high complexity is achieved by tight regulation of multiple proteins including three receptors (insulin receptor (IR), insulin-like growth factor I receptor (IGF-IR), and IGF-II/mannose 6-phosphate receptor (M-6-PR)), three ligands (insulin, IGF-I, and IGF-II), and six known types of circulating binding proteins (insulin-like growth factor binding proteins 1-6 (IGFBP1-6)) (De Meyts et al., 1994; Jones & Clemmons, 1995; Lee & Pilch, 1994). The IGF-IR is a transmembrane tyrosine kinase widely expressed in many human tissues and cell types with high homology to the IR. However, experimental data suggest distinct roles for these two receptors, namely control of cell growth, differentiation and apoptosis by the IGF-IR and the regulation of physiological processes by the IR (Blakesley et al., 1996; Patti & Kahn, 1998; Urso et al., 1999).

The IGF-IR is a heterotetrameric glycoprotein composed of two alpha and two beta subunits, post-transcriptionally linked by disulfide bonds ($\alpha_2\beta_2$). The alpha chain is extracellular, while the beta chain is composed of a short extracellular region, a single transmembrane domain, and a cytoplasmatic portion harboring the catalytic tyrosine kinase domain flanked by two regulatory regions and a juxtamembrane region that serves as a docking site for signaling molecules (Hubbard & Till, 2000). Activation of the receptor is achieved by binding of the specific ligand to the extracellular alpha subunit, triggering autophosphorylation of three tyrosine residues within the kinase domain of the beta subunit (Kato et al., 1993; Murakami & Rosen, 1991).

IGF-I and IGF-II are single-chain polypeptides with sequences 62% identical to pro-insulin. However, they are not proteolytically cleaved but remain linked in their mature form as four peptide domains (Daughaday & Rotwein, 1989; LeRoith et al., 1993). Unlike other peptide hormones, the production and storage of these growth factors is not organ- or cell type-restricted, even though the main fraction originates from the liver. Instead, IGFs may be produced by almost any human cell (Rosen, 1999). The half-lives, transportation and bioavailability of the IGFs circulating at high concentrations in the bloodstream and extracellular fluids are modulated by several high affinity IGFBPs (IGFBP1-6). More than 99% of the circulating IGFs is bound to IGFBPs or can be found in a ternary complex with IGFBPs and a third component, the acid-labile subunit (ALS) (Baxter, 1988). The IGFBP themselves are tightly regulated by tissue specificity,

cell or matrix association, phosphorylation and proteolysis by various proteases (Baxter, 2000; Ferry et al., 1999).

Both IGF-I and IGF-II interact with the IGF-IR, although IGF-I shows a much higher affinity than IGF-II. The closely related insulin, the main ligand for the IR, has an IGF-IR-binding affinity which is less than 1% of that of IGF-I (Denley et al., 2004). The intrinsic receptor for IGF-II, the M-6-PR, differs significantly from the IGF-IR, possesses no tyrosine kinase activity and was reported to target IGF-II for lysosomal degradation, without inducing a specific cell response (Kornfeld, 1992). The ability of the highly homologous IGF-IR and IR to form hybrid receptors by dimerization of their hemi-receptors further increases the complexity of the signaling system. Such IGF-IR/IR hybrid receptors have been reported to influence cell responses by altering the affinities of their growth factor ligands (Pandini et al., 2002).

The activated auto-phosphorylated IGF-IR undergoes major conformational changes, providing docking sites for the recruitment of substrate proteins in order to initiate intracellular signaling cascades. The so far best characterized signaling pathways involve the insulin receptor substrates-1 to -4 (IRS-1 to -4) and the Src-homology collagen protein (Shc) isoforms as adapter substrates. The adapter proteins bind to specific phosphotyrosine residues within the juxtamembrane region of the cytoplasmatic IGF-IR and undergo subsequent tyrosine phosphorylation. Phosphorylation of the IRS adapter molecules on one hand triggers activation of the PI3K/Akt signaling pathway (Myers et al., 1993; Vanhaesebroeck et al., 1997a; Yamamoto et al., 1992), whereas, on the other hand, the Shc adapter activates signaling by the Ras/Raf/MAP-kinase pathway (reviewed in (Vanhaesebroeck et al., 1997a)). Generally, signals controlled by the IGF-IR have pleiotropic effects on cell behavior controlling cell proliferation, differentiation and cell migration, but also regulating the apoptotic machinery (Peruzzi et al., 1999).

2.2.1.1. The Role of the IGF-IR in Human Cancer

In recent years, a growing body of evidence has arisen, suggesting a key role for IGF signaling in various types of human cancer. Since the signals emanating from activated IGF-IR regulate cell proliferation, survival, differentiation and transformation, mechanistic studies have been aimed at defining the role(s) of this receptor in the neoplastic phenotype. While the involvement of the IGF-IR in stimulating cell proliferation was an early finding, a number of studies performed in the last two decades have included experiments aimed at investigating the role of this receptor in the transformation of cells, as well as in metastatic events. Over-expression of the IGF-IR in NIH

3T3 cells lead to a fully transformed phenotype, including anchorage-independent growth and loss of contact inhibition, as well as rapid tumor formation in nude mice (Kaleko et al., 1990). More recently, a novel animal model was generated, involving transgenic expression of a fusion receptor that is constitutively activated by homodimerization (Carboni et al., 2005). The fusion gene was placed under the control of the mouse mammary tumor virus promoter, which drives transcription in the mammary and salivary glands of transgenic mice. The incidence and kinetics of tumor emergence in these animals suggest that the transgene is sufficient to initiate and maintain the transformation process. Transfection of a cell line established from a salivary gland adenocarcinoma with small interfering RNAs against the IGF-IR resulted in a 50% reduction in thymidine incorporation, emphasizing the effect of deregulated signaling via the IGF-IR on cell proliferation (Carboni et al., 2005). Alternatively, other studies have investigated the effect of decreased IGF-IR signaling. Mouse embryo fibroblasts (MEFs) homozygous for a targeted disruption of the *Igfr1* gene showed slower growth than wild-type cells in serum-containing medium and failed to form colonies in soft agar, even when stably transfected with activated Ras, a crucial downstream signaling mediator (Sell et al., 1994). Another approach to study impaired IGF-IR signaling was the generation of LCC6 cells, a metastatic variant of a breast cancer cell line, expressing a C-terminally truncated IGF-IR, which acts as a dominant-negative receptor (Sachdev et al., 2004). These cells showed decreased activation of downstream mediators, such as IRS-1 and IRS-2, as well as Akt. While proliferative responses of these cells to IGF-I or serum were not affected in vitro, they showed decreased anchorage-independent growth. Furthermore, analysis of xenograft tumor growth revealed that in contrast to wild-type cells, cells expressing the dominant-negative IGF-IR did not metastasize to the lungs, although they were equally aggressive locally when compared to wild-type cells (Sachdev et al., 2004).

While no cancer-specific mutations of the IGF-IR or its ligands have been described to date, a plethora of studies have provided evidence for a link between this signaling pathway and the risk of developing cancer (reviewed in (Khandwala et al., 2000)). The most common findings associated with deregulated IGF signaling are over expression of the IGF-IR or the establishment of autocrine or paracrine signaling loops (Table 1). While high expression levels of the IGF-IR have been found in breast and colorectal cancer (Nielsen et al., 2004; Peters et al., 2003), autocrine signaling loops are a more common phenomena, and have been reported in a wide variety of human malignancies (Guo et al., 1995; Nakanishi et al., 1988; Ohmura et al., 1990). Paracrine signaling has mainly been described for breast cancer, where stromal cells have been

shown to produce IGF-I and IGF-II (Gebauer et al., 1998; Yee et al., 1989). Population studies have further highlighted the importance of IGF signaling in some of the most common cancers. The most readily accessible components of the IGF signaling pathway are IGF-I, IGF-II and the IGFBPs, as their circulating concentrations can easily be determined from blood samples. It is important to mention that circulating IGF-I levels vary substantially between normal individuals (Greenspan & Gardner, 2001). Nevertheless, evidence from epidemiological studies has revealed a correlation between elevated IGF-I levels and an increased risk of cancer diagnosis (reviewed in (Pollak et al., 2004)). Although the population studies did not always come to the same conclusions, a recent systematic review of these results led to the interpretation that circulating IGF-I levels are indeed related to a risk of several common cancers (Renehan et al., 2004). The most significant correlation between increased levels of IGF-I and the risk of cancer diagnosis was found for prostate cancer and colorectal cancer (Chan et al., 2002; Giovannucci et al., 2000; Harman et al., 2000; Kaaks et al., 2000; Ma et al., 1999; Palmqvist et al., 2002; Stattin et al., 2000; Wolk et al., 1998). The majority of the studies observed that individuals with elevated levels of IGF-I had an increased risk of developing cancer. It is important to emphasize that the increases detected were modest, and therefore were not always confirmed in population studies, especially if cohort sizes were small (Lacey et al., 2001; Renehan et al., 1999). In the case of breast cancer, elevated levels of IGF-I have only been associated with an increased risk for premenopausal women, while no association between circulating levels and cancer risk was found for postmenopausal women (Hankinson et al., 1998; Keinan-Boker et al., 2003; Krajcik et al., 2002; Toniolo et al., 2000). Although elevated levels of IGF-I were detected in patients newly diagnosed with lung cancer (Yu et al., 1999), population studies were not able to confirm a direct link between plasma levels and cancer risk (London et al., 2002; Lukanova et al., 2001; Spitz et al., 2002). A possible explanation for this inconsistency is the strong influence of carcinogen exposure (e.g. cigarette smoking or asbestos) on the development of lung cancer.

Growth hormone (GH), produced in the pituitary, stimulates production of IGF-I. In patients with acromegaly, where GH levels are increased, retrospective studies suggest that GH hypersecretion modifies the progression of existing malignancies, particularly colon cancer (Orme et al., 1998; Webb et al., 2002). A study performed on GH-treated cancer survivors found no increased risk of disease recurrence or death in these patients. While the overall incidence of secondary malignancies was not increased, survivors of acute leukemia and lymphoma had an elevated number of secondary solid malignancies (Sklar et al., 2002). The relatively marginal effect of

GH/IGF excess on tumor onset and progression might indicate that the auto- and paracrine component of the mechanism is more important than the endocrine.

In summary, both mechanistic as well as epidemiological studies have provided valuable information concerning the role of IGF signaling in human cancers. Since this signaling pathway regulates essential processes such as cell proliferation, survival or differentiation, it might provide targets for the development of promising new therapeutic approach, which could possibly be combined with other classical treatment regimens.

2.2.2. Phosphoinositide 3-Kinases

The PI3Ks are a family of evolutionary conserved lipid kinases, playing a crucial role in controlling a wide variety of intracellular signaling events. PI3Ks phosphorylate phosphatidylinositol (PI) on the D-3 position of the inositol ring, producing distinct second messengers such as PI(3)P, PI(3,4)P₂ and PI(3,4,5)P₃ (PIP₃) (Katso et al., 2001). These lipid products are known to activate diverse target proteins involved in complex signaling cascades, ultimately resulting in the activation of cellular activities comprising cell growth, proliferation, survival and motility.

The family of PI3Ks identified in various species can be subdivided into three main classes (class I-III), based on structural similarity and *in vitro* substrate specificity (Katso et al., 2001) (overview given in Fig. 2). Class I_A includes p110 α , p110 β , and p110 δ , known to form a heterodimeric complex with a p85, p55, or p50 (α or β) regulatory subunit. This adapter subunit contains two SH2 domains mediating their association with activated tyrosine kinase-coupled growth factor receptors (Katso et al., 2001). PIP₃ produced by class I_A PI3Ks activates the protein kinase phosphoinositide-dependent protein kinase-1 (PDK1), inducing the recruitment and activation of the key signal transducer protein kinase B (PKB)/Akt (Vanhaesebroeck & Alessi, 2000). Akt is involved in the regulation of the cell cycle and glucose metabolism through glycogen synthase kinase-3 (GSK-3) (Liang & Slingerland, 2003) and the modulation of cell growth and survival, as well as the control of the translational machinery through the mammalian target of rapamycin (mTOR), the ribosomal protein S6 kinase (S6K) and the 4E-binding protein (4E-BP) (Fingar & Blenis, 2004). Downstream events controlled by Akt further include the control of apoptosis through the regulation of proteins such as forkhead (FKHR), BAD, NF- κ B and murine double minute gene 2 (MDM-2) (Downward, 2004) (overview given in Fig. 1).

Expression studies of the class I_A PI3K isoforms have pointed out an ubiquitous distribution of the subunits p110 α and p110 β in all human tissues, whereas p110 δ is preferentially expressed in leukocytes (Chantry et al., 1997; Vanhaesebroeck et al., 1997a; Vanhaesebroeck et al., 1997b).

The class I_B PI3Ks is made up of one enzyme only, p110 γ , which functions through heterodimer formation with a regulatory subunit p101 (Krugmann et al., 1999) or p84 (Suire et al., 2005). Activation of p110 γ is controlled by receptors capable of activating heterotrimeric guanine nucleotide-binding proteins, termed G-protein coupled receptors (GPCRs) (Krugmann et al., 1999). The PI3K p110 γ is thought to link GPCR signaling to PIP₃ production, governing cell motility in inflammatory cells such as macrophages and to some extent in neutrophils (Hirsch et al., 2000).

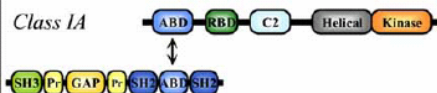
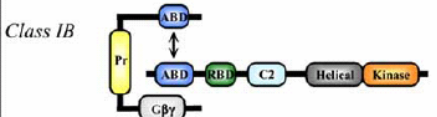


<i>Class I</i>	Subunits Regulatory Catalytic	Substrate Specificity	Activator	Tissue Distribution
<i>Class IA</i> 	p85 α p85 β p55 α p55 γ p50 α	p110 α p110 β p110 δ	PI PIP PIP ₂	Receptor tyrosine kinases Ras p110 α , p110 β : ubiquitous p110 δ : leukocytes
<i>Class IB</i> 	p101 p84	p110 γ	PI PIP PIP ₂	G-protein-coupled receptors (G $\beta\gamma$) Ras leukocytes
<i>Class II</i>				
	PI3KC2 α,β,γ		PI PIP	Receptor tyrosine kinases G-protein-coupled receptors PI3KC2 α,β : ubiquitous PI3KC2 γ : liver
<i>Class III</i>				
	p150	Vps34p analogues	PI	Constitutively active G-protein-coupled receptors (G α)
ABD – Adaptor Binding Domain RBD – Ras Binding Domain C2 – C2 Domain Helical – Helical Domain Kinase – Kinase Domain SH3 – Src Homology Type 3 Domain Pr – Proline-rich Domain GAP – Bcr/Rac GAP Homology Domain SH2 – Src Homology Type 2 Domain G $\beta\gamma$ – G $\beta\gamma$ -binding Site				

Fig. 2: Overview of PI3K isoforms.

(Figure from Doepfner et al.; *Recent Patents of Gene Sequences Relative to the Phosphatidylinositol 3-kinase / Akt Pathway and their Relevance to Drug Discovery* Recent Patents on DNA & Gene Sequences 2007, 1, 9-23 9)

The human class II of PI3Ks comprises the three isoforms PI3KC2 α , PI3KC2 β and PI3KC2 γ (Katso et al., 2001). The hallmarks of class II family members are a substrate specificity restricted to PI and PI(4)P *in vitro*, and a C-terminal C2 domain. Although the precise cellular function of these enzymes remains generally unknown, recent reports have described class II PI3Ks as downstream transducers of activated polypeptide growth factor receptors (Arcaro et al., 2000; Brown et al., 1999). The class III PI3K includes a homolog of the yeast vesicular protein-sorting protein Vsp34 (Schu et al., 1993) and its major function is in intracellular trafficking events (Wurmser et al., 1999).

2.2.2.1. Inhibition of PI3K Signaling

As the PI3Ks have been identified as playing critical roles in distinct cellular signaling processes, a precise understanding of these kinases, their substrates, products and effectors is of particular interest. Anomalies in signaling cascades have been described in various human diseases and the knowledge of their components is of high importance in the search for therapeutic, diagnostic and screening applications. A number of attempts have been made to better understand the PI3Ks in general, as well as to gain insight into the relevance and specificity of the different isoforms. The first selective pharmacological PI3K inhibitors to have been described are wortmannin (Arcaro & Wymann, 1993; Powis et al., 1994), a compound that was originally isolated from soil bacteria and is toxic to fungi, and LY294002 (Vlahos et al., 1994), a morpholino derivative of quercetin, a naturally occurring bioflavonoid and broad spectrum kinase inhibitor. Both compounds have been shown to inhibit cell growth at concentrations that would be expected to inhibit class I PI3Ks. However, as these pharmacological inhibitors display little selectivity within the family of the PI3Ks and might moreover affect other kinases, further research has been aimed at developing compounds with improved specificity and pharmacokinetic properties.

2.2.2.2. Gene-Targeting Strategies

Gene-targeting strategies have been aimed at deleting specific PI3K isoforms and have uncovered key roles of the different enzymes in immunity, metabolism, cardiac function, cell proliferation and cancer susceptibility. Different knock-out mice have been generated with targeted deletions of genes encoding PI3K regulatory and catalytic subunits and have been phenotypically analysed (Vanhaesebroeck et al., 2005).

A knock-out mouse deleting the gene of the PI3K class I_A catalytic subunit p110 α has been generated by targeting the p85-binding domain of the *PIK3CA* gene, leading to the loss of expression of this specific isoform (Bi et al., 1999). The *PIK3CA*^{del/del} embryos showed a clear developmental delay and died between days 9.5 and 10.5 of embryonic development (Bi et al., 1999). In embryos missing the p110 α enzyme, a profound proliferation defect could be observed, which has further been supported by a failure in replication of p110 α -deficient fibroblasts in culture medium, even when supplemented with growth factors. As the developmental period between E9.5 and E10.5 is known for increased cellular proliferation, growth, and differentiation, it has been hypothesized that the intrauterine death of *PIK3CA*^{del/del} embryos at this stage is caused by the incapacity to provide the increased demand in proliferation signals maintained by PI3K signaling through the p110 α isoform (Bi et al., 1999). Moreover, mice deficient in the p110 α subunit displayed multiple vascular defects (Lelievre et al., 2005). A role in the control of cell growth by p110 α was further highlighted by an increase in heart size in transgenic mice expressing constitutively active p110 α and a decrease in heart size by expression of a dominant-negative mutant form of this PI3K isoform in the heart (Shioi et al., 2000). The interpretation of knock-out data, however, has been complicated by the observation of an upregulation of other PI3K subunits after the deletion of one specific isoform. *PIK3CA*^{del/del} homozygous embryos apparently increased the expression of the PI3K class I_A regulatory subunit p85/p55 raising the question of a contributing phenotypical effect by these adapter proteins. Further insight into the function of p110 α has been given by the generation of mice carrying a knock-in mutation (D933A) that abrogates the p110 α kinase activity (Foukas et al., 2006). Homozygosity for this mutation resulted in embryonic lethality while heterozygosity led to impaired signaling via the IRS proteins, key mediators of insulin, IGF-I and leptin action. As a result, the mutant mice displayed reduced somatic growth, hyperinsulinaemia, glucose intolerance, hyperphagia, and increased adiposity. Another study recently defined the p110 α subunit as the critical lipid kinase required for insulin signaling in adipocytes and myotubes (Knight et al., 2006). The uncovering of p110 α as a key intermediate in metabolic signaling raises concerns about potential mechanism-based side-effects and the therapeutic use of PI3K inhibitors .

The biological function of the PI3K class I_A catalytic subunit p110 β has been studied by a partial deletion allele knock-out mouse (Bi et al., 2002). Targeting of this specific isoform resulted in very early embryonic lethality at the homozygous state. Zygotes with the *PIK3CB*^{del/del} genotype

were nonviable very early after fertilization, leading to a deficiency of such embryos even at the blastocyst stage (Bi et al., 2002). Crossbreeding studies of p110 β knock-out mice with p110 α -deleted mice did not reveal a possible redundant function of these two class I_A catalytic subunits. However, a possible overlap in functions that might be manifested in subtle phenotypical abnormalities could not be ruled out so far (Bi et al., 2002).

PI3K class I_A catalytic subunit p110 δ -deficient mice have been described by three different groups (Clayton et al., 2002; Jou et al., 2002; Okkenhaug et al., 2002). These studies revealed a major function of p110 δ primarily in B and T lymphocytes and a failure of the knock-out mice to mount normal immune responses. The mice lacking p110 δ showed a reduction in the amount of B1 and marginal zone B cells as well as lowered serum levels of immunoglobulins (Clayton et al., 2002). Furthermore, antigen receptor signaling in B and T cells was impaired and the mice were prone for the development of inflammatory bowel disease (Okkenhaug et al., 2002). However, despite the high level of p110 δ expression in hematopoietic tissues, no significant differences have been found between wild-type and p110 δ -deficient mice in the number or morphology of red blood cells and peripheral leukocytes, including neutrophils, eosinophils, basophils, monocytes, and lymphocytes, nor hemoglobin levels (Jou et al., 2002).

Knock-out mice of the PI3K class I_B catalytic subunit p110 γ have been characterized by three different groups (Hirsch et al., 2000; Li et al., 2000; Sasaki et al., 2000b), describing phenotypes mainly affecting components of the innate immune response. Mice lacking p110 γ showed an accumulation of defective neutrophils, exhibiting failure in their migratory capacity and reduced thymic cellularity. Moreover, chemoattractant-stimulated signal transduction was inhibited by impairment of PIP₃ production in p110 γ -deficient cells (Sasaki et al., 2000b). In contrast to p110 δ , the deletion of p110 γ resulted in no effect on B cells. Instead, this isoform appeared to regulate proliferation and cytokine production of T lymphocytes (Sasaki et al., 2000b). In view of the impaired migration capability of p110 γ knock-out macrophages towards a wide range of chemotactic-stimuli, a crucial role for macrophage accumulation in the inflammatory response was furthermore suggested (Hirsch et al., 2000). Phenotypical analysis of mice expressing a kinase-dead p110 γ only partially reproduced the phenotype of knock-out animals (Patrucco et al., 2004). Whereas both mice exhibited an identical impairment in innate immune reactions, the p110 γ -deficient mice additionally showed a basal enhancement of cardiac contractility and cardiac tissue damage upon pressure overload. It is therefore suggested that p110 γ possesses a

kinase-independent activity controlling cardiac responses. A role of p110 γ in the control of heart function has already been described by Crackower et al. (Crackower et al., 2002). These studies elucidated p110 γ as a negative regulator of cardiac contractility through the inhibition of cAMP production.

Regarding the regulatory PI3K subunits, gene-targeting strategies have been aimed at disrupting the adapter subunits p85 α , its splice variants p55 α and p50 α , as well as p85 β . Ablation of the whole gene *PIK3R1*, which encodes p85 α and the mentioned splice variants, resulted in perinatal lethality (Fruman et al., 2000). However, disruption of the *p85 α* gene only lead to an impaired B cell development, a reduction in the number of mature B cells, reduced B cell proliferative responses and no T cell-independent antibody production (Fruman et al., 1999). Homologous deletion of the adapter subunit *p85* gene resulted in a growth reduction of the knock-out mice compared to their wild-type littermates (Ueki et al., 2002). Surprisingly, muscle and adipocyte tissues of both, the p85 α and p85 β knock-out mice exhibited increased insulin-stimulated PI3K pathway activation and enhanced translocation of the glucose transporter isoform-4 to the plasma membrane, as well as hypoglycemia with decreased plasma insulin (Fruman et al., 2000; Ueki et al., 2002). Moreover, the mice showed enlarged muscle fibres, brown fat necrosis and calcification of cardiac tissue (Fruman et al., 2000).

2.2.2.3. PI3K and Diseases

As the PI3Ks are known to be involved in a wide spectrum of control mechanism within the cell, dysregulation of their function has been linked to various human diseases. Key roles of the PI3Ks have been described in the formation of tumors, metastasis, chronic inflammation, allergy and cardiovascular disease.

The importance of PI3K signaling in human cancer is highlighted by the fact that there are numerous oncogenes and tumor suppressor genes whose dysregulation advantages PI3K signaling and promotes malignant properties of cells (Vivanco & Sawyers, 2002). A prominent finding in this context are mutations in the tumor suppressor gene phosphatase and tensin homolog (PTEN) that have been described in various human tumors (Aggerholm et al., 2000; Ali et al., 1999; Katso et al., 2001; Vivanco & Sawyers, 2002). PTEN is a phosphatase that antagonizes the action of PI3K by dephosphorylating the D-3 position of polyphosphoinositides (Maehama & Dixon, 1998). The DNA sequence copy number of *PIK3CA*, the gene encoding the

p110 α catalytic subunit of the PI3K located on chromosome 3q26, is frequently increased in ovarian cancers (Shayesteh et al., 1999). Moreover, recent reports have described activating mutations in the *PIK3CA* gene in a variety of other human cancers, including, breast, colon and medulloblastoma (Kang et al., 2005; Samuels et al., 2004). Although mutational alterations have predominantly been characterized for p110 α so far, an increase in p110 β activity has also been found in human colon cancer biopsies and adenocarcinoma cell lines (Benistant et al., 2000). Furthermore, a knock-down analysis of p110 β in a prostate cancer mouse model suggested a requirement of this PI3K isoform for the formation of metastasis (Czauderna et al., 2003).

Gene-targeting strategies have furthermore uncovered a role of p110 γ in colorectal adenocarcinoma (Sasaki et al., 2000a). Lack of p110 γ significantly increased the incidence rate for spontaneous development of multifocal carcinomas and invasive adenocarcinoma in the colon of mice. In humans, protein expression analysis of p110 γ revealed a loss of this protein in a high number of colon cancer cell lines as well as in primary adenocarcinomas isolated from the colon of human patients (Sasaki et al., 2000a).

As shown by different studies (Laffargue et al., 2002; Sasaki et al., 2000b), p110 γ also plays a pivotal role in mediating leukocyte chemotaxis and activation, as well as mast cell degranulation, thus suggesting an involvement in inflammatory diseases. A specific contribution of the p110 γ -PI3K isoform to inflammation is supported by a recent study pointing out a protection of p110 γ -deficient mice from rheumatoid arthritis (RA) (Camps et al., 2005). The mice were largely protected against collagen II-specific antibody-induced arthritis, correlating with the defective neutrophil chemotaxis in this knock-out model (Camps et al., 2005). Moreover, treatment of different RA mouse models with orally active small-molecule inhibitors of p110 γ suppressed the progression of the joint inflammation and damage in these mice (Camps et al., 2005). Other studies, however, have described a positive role of the PI3Ks in the inflammatory response. In RA, the anti-inflammatory cytokine IL-10 is spontaneously produced by macrophages and infiltrating blood lymphocytes in the rheumatic joint (Brennan & Foey, 2002). An involvement of PI3K signaling in the regulation of IL-10 is known (Crawley et al., 1996) and further analysis have demonstrated that the inhibition of PI3K signaling suppressed the production of this cytokine (Foey et al., 2002).

The PI3K isoform p110 δ has been shown to contribute to the inflammatory response as well (Clayton et al., 2002). Recent studies further supported this finding describing a contribution to

allergen-IgE-induced mast cell activation and vascular permeability which is a common characteristics of chronic inflammations such as asthma (Lee et al., 2006a). Pharmacological inhibition of p110 δ resulted in a significant reduction of serum levels of IgE, attenuation of airway inflammation and hyperresponsiveness, by preventing vascular leakage in murine asthma models (Lee et al., 2006a; Lee et al., 2006b).

Gene knock-out of the class I_A regulatory subunits in skeletal muscles of mice resulted in a significant reduction in muscle weight and fiber size. Moreover, these mice exhibited muscle insulin resistance and whole-body glucose intolerance (Luo et al., 2006). The p85 regulatory subunits are therefore thought to act as critical mediators of PI3K signaling in the regulation of muscle growth and metabolism and furthermore, to make an important contribution to symptoms of hyperlipidemia associated with human type 2 diabetes (Luo et al., 2006). Diabetes is associated with vascular complications, including the impairment of vascular function and alterations in the reactivity of blood vessels to vasoactive agents (Jarrett, 1989). It has been shown that PI3K signaling plays a role in vascular growth, proliferation and apoptosis and is implicated in modulating vascular smooth muscle cell contractility (Zdychova & Komers, 2005). A recent study demonstrated that selective inhibition of PI3K attenuated the development of diabetes-induced abnormal vascular reactivity in the carotid arteries of diabetic rats (Yousif et al., 2006).

The growing understanding of the biological functions of PI3Ks opened insights into the interconnection of signaling events and cellular actions and made these kinases interesting targets in clinical and research areas.

2.2.3. Alteration of RTK Signaling in AML

The increasing understanding of the pathogenesis of AML uncovered multiple genetic abnormalities necessary for the development of the disease. In the classical ‘two hit’ model, the second hit is thought to be caused by alterations in RTK signaling and various aberrantly regulated pathways have been described so far. Basically, there is an oncogenic potential in every receptor with tyrosine kinase activity. Structural modifications can lead to constitutive activation of RTKs, subversion of molecular control mechanisms and alterations in signal transduction. Deletions within the extracellular ligand binding domain alters ligand responsiveness, or eliminates negative control mechanisms that this structure might exert on the kinase domain. Even point mutations are able to induce overall ligand-independent conformational alterations

and hence activation of RTKs. Besides genetic alterations, over-expression of the wildtype receptor and/or autocrine receptor activation are known to play an important role in aberrant signal transduction.

FLT3 is the most frequently mutated gene in AML. About one third of all patients show either internal tandem duplications (ITDs) within the juxtamembrane domain (Nakao et al., 1996) of FLT3, or mutations within the activation loop, predominantly at position D835 (Yamamoto et al., 2001). FLT3 is a transmembrane receptor that has a crucial role in normal haematopoiesis. By signaling through the Ras/MAPK pathway the receptor exerts an important function in the control of cell proliferation. FLT3-ITD as well as activating loop mutations result in constitutive activation of the tyrosine kinase activity and of the whole signaling network (Gilliland & Griffin, 2002; Stirewalt & Radich, 2003).

Activating point mutations in the kinase domain of the human colony-stimulating factor (M-CSF or CSF-I) receptor FMS occur in 5-20% of patients with AML (Ridge et al., 1990). FMS is a cell surface RTK and specific point mutations in this receptor have been implicated in neoplastic transformation by inducing ligand independence and constitutive activation of the tyrosine kinase activity. The mutation at codon 969 of FMS is thought to alter a negative regulatory site of the receptor and to up-regulate the response to ligand binding, conferring a growth advantage to the cell (Ridge et al., 1990). Co-expression of M-CSF together with FMS has been described for a small subset of AML patients, implicating autocrine stimulation of the wildtype receptor (Rambaldi et al., 1988). Moreover, patients with myeloplastic syndrome harboring FMS mutations were shown to have a significantly increased frequency of transformation to AML (Padua et al., 1998).

Mutations in the RTK c-Kit have been preferentially associated with AML exhibiting either an inv(16) or a t(18;21) karyotype (Beghini et al., 2000). c-Kit encodes a transmembrane receptor that is activated SCF. Studies have shown that the levels of activation of c-Kit correlate with the rate of proliferation of myeloid leukemia cells and that receptor over-activation contributes to the excessive proliferation and aberrant differentiation of AML cells (Kuriu et al., 1991).

Mutations in the *RAS* gene family have been described in about one fourth of AML cases, predominantly in N-Ras, but also in K-Ras and, although very rarely, in H-Ras (Bartram et al., 1989; Farr et al., 1988). Primarily, mutations were found to affect the conversion of the active Ras-GTP form to the inactive Ras-GDP form leading to constitutively activated Ras and enhanced downstream signaling. Besides, over-activation of downstream transducers have been described as a result of FLT-ITD affecting the autonomous growth of AML cells (Hayakawa et al., 2000).

Moreover, increased activation of the Ras/MAPK pathway has been shown to be caused by a commonly occurring chromosomal translocation. BCR-ABL is a chimeric oncoprotein that binds to Grb-2, the substrate protein known to link receptor tyrosine kinases to Ras signaling. Coupling of BCR-ABL-Grb-2 to SOS subsequently induces activation of the signaling pathway (Pendergast et al., 1993).

FLT-ITD has furthermore been associated with increased activation of the Janus protein tyrosine kinase (JAK)/signal transducer and activator of transcription (STAT) pathway. Constitutive tyrosine phosphorylation of the transcription factor STAT occurs in approximately 70% of AML cases, either through autophosphorylation of RTKs, or due to autocrine growth factor production (Birkenkamp et al., 2001). STAT signaling involves the control of diverse biological processes including cell proliferation, differentiation, development, and survival. Abnormal STAT signaling has been implicated in oncogenesis (Bromberg et al., 1999). Beside its role in FLT3 signaling, the JAK/STAT pathway has been associated with c-Kit-mediated ligand-independent survival and proliferation of AML cells. In fact, the c-Kit mutation Asp⁸¹⁶ has been found to constitutively activate the JAK/STAT pathway (Ning et al., 2001). Moreover, chromosomal translocations resulting in the fusion of the *JAK2* and the *TEL* gene have been described in human leukemias. The TEL-JAK2 fusion protein confers constitutive tyrosine kinase activity and cytokine-independent proliferation to hematopoietic cells (Lacronique et al., 1997; Peeters et al., 1997).

An increasing body of evidence suggests a role of signaling by the IGF-IR through the PI3K/Akt/mTOR cascade in AML. IGF-I together with other cytokines have been described to be important for AML cell growth (Shimon & Shpilberg, 1995) and autocrine IGF-I production has been suggested to influence drug resistance in an AML cell line (Neri et al., 2003). Activation of the PI3K/Akt signaling pathway has furthermore been detected in blast cells from AML patients contributing to survival and proliferation of these cells (Grandage et al., 2005; Xu et al., 2003).

2.2.4. Targeting RTK Signaling in AML

Significant progress has been made over the past decades in the treatment of AML. Insights into the pathogenesis, detection of cytogenetic markers and classification of the disease have facilitated the definition of optimal therapy conditions. However, overall survival rates are still unsatisfactory and are highly influenced by complications resulting from therapy. Improvement of the current therapeutic approaches is thus urgently needed and major advances are hoped to arise from a more targeted therapy strategy. The increasing understanding of the high impact of receptor tyrosine

kinase signaling in AML and the discovery of specific alterations and dysregulation of signaling cascades sparked interest in specifically targeting RTK signaling in this disease. Besides, the growing number of molecularly targeted drugs displaying promising results in other human cancers further brought the focus onto targeting RTK signaling in AML and led to a plethora of preclinical and clinical trials.

Given the fact that a large number of AML cases show constitutive activation of one or more RTKs, the use of small molecule inhibitors targeting their tyrosine kinase activity appears to represent a great promise. The remarkable activity of imatinib mesylate (Gleevec) targeting the BCR-ABL fusion protein in chronic myeloid leukemia (CML) (Druker, 2003) further developed the interest in the field of molecularly-targeted therapies in leukemia. The major focus in AML has been directed towards FLT3 and c-Kit. The uncovering of other receptors important for AML cell biology and the development of a plethora of new small molecule inhibitors, however, has broadened the field of targeted research in this malignancy.

2.2.4.1. FLT3

FLT3 is a class III receptor tyrosine kinase expressed by immature hematopoietic cells. Its expression is important for the normal development of stem cells and the immune system (Gilliland & Griffin, 2002). The FLT3 ligand (FL) is a transmembrane protein that can be released as a soluble homodimeric protein. Both the membrane-bound, as well as the soluble form of FL are able to activate the tyrosine kinase activity of the receptor, and, synergistically with other hematopoietic growth factors, to induce proliferation of hematopoietic progenitor cells (Lyman & Williams, 1995). Expression of FLT3 is found in the majority of AML patients and a crucial role of this receptor in the survival and proliferation of leukemic blasts has been described in various studies (Carow et al., 1996). Molecular alterations in the FLT3 receptor were first described in 1996 by Nakao et al (Nakao et al., 1996). Reverse transcriptase-polymerase chain reaction (RT-PCR) analysis revealed longer transcripts within the juxtamembrane domain of FLT3 in a large proportion of AML patients. This finding led to the discovery of commonly occurring ITDs within that region. A plethora of subsequent studies uncovered an overall frequency of FLT-ITDs of about one fourth of all cases of AML. More recently, in an additional cohort of AML patients, mutations within the activation loop of the kinase domain of FLT3 were found (Griffin, 2001; Yamamoto et al., 2001). Point mutations commonly occur at position 835 (Asp835) and have been reported in around 7% of AML cases so far. Taken together, the global incidence rate of altered FLT3 function

in AML patients caused either by FLT3-ITD, or by FLT3 activation loop mutation, represents almost one third of all cases. The high prevalence of activating mutations in this receptor therefore makes FLT3 one of the most interesting targets for molecularly based therapies.

Indoline tyrosine kinase inhibitors are known to inhibit the tyrosine kinase activity of a number of RTKs, such as FLT3, c-Kit, PDGFR, VEGFR or the FGFR. Pre-clinical studies have examined the effect on the FLT3 receptor and its signaling and initial clinical trials have been aimed at evaluating their biological activity in AML patients (Fiedler et al., 2003; Fiedler et al., 2005; Giles et al., 2003; Mesters et al., 2001; O'Farrell et al., 2003b; O'Farrell et al., 2004; Smolich et al., 2001; Yee et al., 2002). SU5416 and the related compound SU5614 were shown to inhibit the kinase activity of both the wildtype FLT3, as well as the mutated receptor. Furthermore, both compounds inhibited downstream signaling via the MAPK and the STAT pathway, markedly decreased cellular proliferation and increased apoptosis in AML (Smolich et al., 2001; Yee et al., 2002). In phase II clinical studies evaluating SU5416 in elderly AML patients, or patients with relapsed and/or refractory disease, single agent treatment had only minimal clinical activity. Partial remission and hematopoietic improvement was seen, however, in a small cohort of patients and these improvements were of short duration (Fiedler et al., 2003; Giles et al., 2003; O'Farrell et al., 2004). A significant decrease in blast cell count down to undetectable levels and stable remission after administration of SU5416 has only been described in a single case study of a patient with relapsed AML (Mesters et al., 2001). SU11248 is another oral multitargeted kinase inhibitor that targets FLT3 together with other RTKs. Pre-clinical studies showed *in vitro* activity against the wildtype, as well as the mutated FLT3 receptor and *in vivo* activity against xenograft FLT3-ITD AML tumors in engraftment mouse models (O'Farrell et al., 2003a). Phase I clinical trials underlined the action of SU11248 against the FLT3 kinase activity. Monotherapy of SU11248, however, only induced partial remission in a small number of AML patients for a short duration (Fiedler et al., 2005; O'Farrell et al., 2003b).

PKC412 is small molecule FLT3 inhibitor that was identified and characterized by Weisberg et al. (Weisberg et al., 2002). PKC412 selectively induces G1 cell cycle arrest and apoptosis in cell lines expressing mutant FLT3 by directly inhibiting its kinase activity. Progression of leukemia was inhibited in FLT3-ITD transduced mouse models making this inhibitor a valuable candidate for clinical trials in patients carrying mutant FLT3 receptors (Weisberg et al., 2002). Subsequent pre-clinical studies highlighted the potential use of this inhibitor against FLT3 kinase activity and reported an effect of PKC412 on the phosphorylation of the downstream targets Akt, Erk and

STAT5 (George et al., 2004). A phase II clinical trial in a small cohort of patients showed significant clinical benefit and a 50% decrease in peripheral blast counts in most patients with mutated FLT3, in line with inhibition of receptor autophosphorylation (Stone et al., 2005).

Levis et al. characterized CEP-701, an indolocarbazole derivative with potent activity against autophosphorylation of wild-type and constitutively activated FLT3 (Levis et al., 2002). CEP-701 inhibited the FLT3 downstream targets Erk and STAT5 and induced a cytotoxic effect in AML patient cells harboring FLT3-ITDs. Furthermore, CEP-701 prolonged survival in a mouse model of FLT3-ITD leukemia (Levis et al., 2002). A recent study substantiated the potential of CEP-701 in reducing cell viability and FLT3 phosphorylation in a large number of patient cells (Knapper et al., 2006b). *In vivo* hematological activity of CEP-701 has been studied in clinical phase I/II trials. Treatment of patients with refractory, relapsed, or poor prognosis AML expressing FLT3-activating mutations with CEP-701 revealed biological activity and a measurable clinical response including reduction in peripheral and bone marrow blood blasts in some patients (Smith et al., 2004). The clinical response was more pronounced in patients with mutated FLT3 than in those expressing the wild-type receptor (Knapper et al., 2006a).

Recently, tandutinib (MLN518) was identified as a novel, relatively specific FLT3 antagonist (Deangelo et al., 2006). Pre-clinical studies showed activity against FLT-ITD autophosphorylation and inhibition of AML cell proliferation *in vitro* (Kelly et al., 2002). A clinical phase II study reported evidence of antileukemic activity with a decrease in both peripheral and bone marrow blast count in a small cohort of patients treated with tandutinib (Deangelo et al., 2006).

2.2.4.2. c-Kit

c-Kit encodes another transmembrane protein with tyrosine kinase activity and is a proto-oncogene thought to play an important role in normal hematopoiesis. c-Kit expression has been detected in a large number of hematopoietic cell lines, in primary blasts of human AML patients, but to a much lower level in normal bone marrow cells (Wang et al., 1989). Tyrosine phosphorylation and activation of c-Kit is induced by binding of SCF and results in proliferation of human leukemia blast cells in a substantial fraction of AML cases. The constitutive, ligand-independent activation of c-Kit found in leukemic cells suggests that this receptor is involved in the excessive proliferation and aberrant differentiation of these cancer cells (Kanakura et al., 1993). Moreover, a direct correlation has been found between the levels of c-Kit tyrosine phosphorylation and the proliferation rate in AML cell lines (Kuriu et al., 1991). Mutations in c-Kit are thought to be

exclusively associated with core binding factor leukemias (CBF-AML). In addition to mutations within the tyrosine kinase domain of c-Kit at position 816, insertions and deletions have been described (Care et al., 2003; Gari et al., 1999).

Imatinib, also known as STI571 or Gleevec, has been shown to be a very promising small molecule inhibitor targeting the tyrosine kinase activity of the BCR-ABL fusion protein commonly found in CML. Moreover, the inhibitor was shown to effectively inhibit the PDGFR as well as c-Kit (Heinrich et al., 2000). Imatinib prevented autophosphorylation of c-Kit and activation of the downstream signal transducers MAPK and Akt. Furthermore, treatment of an AML cell line expressing the BCR-ABL fusion protein induced apoptosis and significantly increased the sensitivity to chemotherapeutical agents (Fang et al., 2000). In c-Kit-positive primary AML patient blasts, however, Imatinib exerted only marginal effects on cell growth (Scappini et al., 2001). Nevertheless, a pre-clinical study analyzing cells expressing c-Kit mutants cloned from AML patients reported a dose-dependent increase in apoptosis upon treatment with the inhibitor (Cammenga et al., 2005). In a first clinical phase II trial of patients with refractory or recurrent AML, Imatinib as single agent did not induce any significant beneficial responses (Cortes et al., 2003). A later phase II pilot study including a small cohort of c-Kit-positive patients, however, showed high efficacy of Imatinib resulting in the inhibition of c-Kit tyrosine phosphorylation and promising results in a subset of patients meeting the criteria for complete hematological remission (Kindler et al., 2004). Consistently, different case studies have described a potential benefit of Imatinib treatment for c-Kit-positive AML patients and carriers of specific c-Kit mutations (Cairolì et al., 2005; Ito et al., 2005; Jentsch-Ullrich et al., 2004; Kindler et al., 2003; Pompetti et al., 2006; Schittenhelm et al., 2003; Viniou et al., 2004; Yamaguchi & Konishi, 2003).

2.2.4.3. IGF-IR

The IGF-IR is a transmembrane tyrosine kinase widely expressed in many human tissues and cell types, with high homology to the IR. Activation of the receptor is achieved by binding of the IGFs to the extracellular domain, triggering autophosphorylation of three tyrosine residues within the kinase domain (Kato et al., 1993). In AML, signaling by the IGF-IR has not yet been extensively studied, however, expression of the IGF-IR was reported in human AML cells (Hizuka et al., 1987; Sukegawa et al., 1987). While mutations resulting in constitutive tyrosine kinase activity of the IGF-IR have not been described to date, over-expression of the receptor and/or the establishment of autocrine loops involving the ligands IGF-I and IGF-II have been reported in various human

cancers (Khandwala et al., 2000). The importance of IGF-I as a growth factor in combination with other cytokines has been described in human AML cells (Shimon & Shpilberg, 1995). A recent study further underlined the importance of IGF-IR signaling by showing an association between increased expression of IGF-I and resistance to the chemotherapeutic agent Cytarabine (Ara-C) in leukemia (Abe et al., 2006). Gene expression profiling of Ara-C-resistant human myeloid leukemia cells revealed an up-regulation of IGF-I. Subsequent analysis of AML cases uncovered higher IGF-I expression in patients with refractory disease after Ara-C therapy compared to patient cells analyzed at diagnosis (Abe et al., 2006). Consistently, a role of autocrine IGF-I production in drug resistance was previously suggested in an AML cell line (Neri et al., 2003). In addition, IGF-I signaling is known to play a crucial function in other hematological malignancies such as multiple myeloma (MM) (Yasui et al., 2006), and several anti-IGF-IR experimental therapies have been shown to inhibit multiple myeloma proliferation *in vitro* and *in vivo* (Mitsiades et al., 2004). Blocking the IGF-IR in the Ara-C resistant myeloid cell line described above inhibited cell growth and led to the induction of apoptosis, suggesting that the IGF-IR and its downstream signaling pathways may provide valuable novel targets to overcome Ara-C resistance in AML (Abe et al., 2006).

The increasing understanding of the importance of the IGF-IR signaling pathway in AML cell proliferation, viability and drug-resistance makes this system an interesting new molecular target for cancer therapy. Promising small molecule inhibitors have been generated and a wide variety of strategies are now available to target IGF signaling (Guerreiro et al., 2006).

2.2.5. Downstream Signal Transducers

Targeting pathways downstream of RTKs is another approach to down-regulate an overactivated signaling system with significant therapeutic advantages. The growing understanding of the complexity of RTK signaling networks has indeed revealed a number of promising target proteins contributing to altered signaling in cancer cells. As described above, deregulation of RTKs frequently induces over-activation of the PI3K/Akt, Ras/MAPK and JAK/STAT cascades in AML. Inhibitors targeting various signal transducer proteins including Akt and mTOR, Ras and MEK have been developed and are being tested in preclinical studies in various human cancers including AML.

2.2.5.1. PI3K/AKT

The PI3K pathway is essential for different physiological processes including transcription, translation, cell cycle progression and apoptosis. The PI3K cascade is the signaling system most frequently targeted by genetic alterations in human cancer, along with p53 and the retinoblastoma pathway. Genomic aberrations such as amplifications, rearrangements and mutations induce activation of the pathway, thus providing the tumor cells with a strong growth advantage (Osaki et al., 2004). The PI3Ks are a family of eight enzymes in humans, which are subdivided into 3 classes (I-III), based on sequence homology and substrate specificity (Vanhaesebroeck et al., 1997a). Class I_A and class II PI3Ks transduce signals from activated RTKs. These PI3Ks are also activated by oncogenic mutants of Ras, such as N- and K-Ras, which are found in AML. Several downstream targets of PI3K transduce their proliferative and anti-apoptotic signals, including Akt/PKB, PDK-1, FKHR, GSK-3 β , TSC1 and TSC2, BAD, Rheb, mTOR, S6K, 4E-BP. The importance of the PI3K/Akt axis in AML cell progression has been highlighted by several studies (Kubota et al., 2004; Min et al., 2003; Xu et al., 2003; Zhao et al., 2004). Constitutive activation of PI3K was found in more than 50% of AML cases and the activation of Akt was significantly higher in spontaneously proliferating AML cells than in cells that did not proliferate spontaneously (Kubota et al., 2004). Moreover, constitutive phosphorylation of Akt at Ser473 negatively correlated with the overall survival rate of AML patients (Min et al., 2003).

The inhibition of PI3Ks by the generic inhibitor LY294002 resulted in reduced Akt kinase activity, dephosphorylation of Akt and BAD and an increase in apoptosis in AML cell lines (Xu et al., 2003; Zhao et al., 2004). PI3K inhibition in primary AML blasts resulted in significantly reduced clonogenic growth (Zhao et al., 2004). Moreover, inhibition of the pathway sensitized AML cells to chemotherapy-induced apoptosis (O'Gorman et al., 2000). A recent study examined the anti-leukemic effect of the novel small-molecule multiple kinase inhibitor KP372-1 in AML (Zeng et al., 2006). KP372-1 potently inhibited the kinase activity of Akt, PDK1 and FLT3 in a dose-dependent manner. The inhibitor induced pronounced apoptosis in AML cell lines and primary blasts. Furthermore, KP372-1 decreased the colony-forming ability of primary AML blasts with minimal cytotoxic effects on normal progenitor cells (Zeng et al., 2006). The finding that normal hematopoietic progenitor cells were less affected by inhibitors targeting PI3K signaling than AML cells was previously described by others (Xu et al., 2003; Zhao et al., 2004) and further supports the feasibility of targeting this fundamental signal transduction network for AML therapy. The use of generic non-selective inhibitors such as LY294002 or wortmannin, however, has been shown to

cause severe side effects in xenograft models (Cheong et al., 2003) and the identification of more selective inhibitors is required. Recently, IC78114, a class I_A PI3K p110 δ -selective inhibitor, was shown to efficiently suppress constitutive as well as FLT3-stimulated activation of Akt in AML blasts to the same extent as the non-selective generic PI3K inhibitor LY294002 (Sujobert et al., 2005). Moreover, the isoform-selective inhibitor suppressed AML cell proliferation without affecting the proliferation of normal progenitor cells.

2.2.5.2. mTOR

mTOR is a key regulator of growth and survival and is activated by various RTK receptors. Once activated, the serine/threonine kinase phosphorylates its downstream targets, the ribosomal S6K and 4E-BP. Aberrant activation of the mTOR signaling pathway in AML cells is supported by the finding of constitutive phosphorylation of S6K and 4E-BP in the majority of AML samples (Recher et al., 2005).

Rapamycin is a well known inhibitor of mTOR and is used clinically as an immunosuppressant and antiproliferative agent (Hidalgo & Rowinsky, 2000; Schreiber, 1991). Studies evaluating the effect of rapamycin in AML cells have reported marked activity of the inhibitor in down-regulating phosphorylation of S6K and 4E-BP (Hahn et al., 2005; Mohi et al., 2004; Recher et al., 2005) and inhibiting cell growth by blocking the cell cycle, particularly in very immature AML cell lines (Recher et al., 2005). Treatment of primary AML blasts with the mTOR inhibitor impaired their clonogenic properties, while normal hematopoietic progenitors were not affected. Moreover, rapamycin synergistically induced apoptosis in conjunction with protein kinase inhibitors (Hahn et al., 2005; Mohi et al., 2004). A pilot clinical study comprising a small number of patients with refractory, relapsed or poor prognosis AML showed significant responses suggesting that rapamycin could be of clinical interest for AML treatment. Partial remission or stabilization of the disease was reported in five out of nine patients analyzed (Recher et al., 2005). Evaluation of RAD001 (Everolimus), a rapamycin derivative, revealed only marginal effects on AML cell growth as a single-agent. Combined treatment together with the chemotherapeutic agent Ara-C, however, significantly enhanced the response of AML cells to the cytotoxic drug (Xu et al., 2003).

2.2.5.3. RAS/RAF/MEK/ERK

The MAPK signaling cascade is yet another important system that integrates extracellular stimuli and transduces them to cellular responses, such as proliferation, differentiation and survival. RTKs

signal through activation of the small GTP-binding protein Ras via the adapter molecule Grb2 and the guanine nucleotide exchange factor son of sevenless (SOS). Sequential stimulation of the cytoplasmatic proteins Raf, MEK and Erk, collectively known as MAPKs, finally results in the regulation of gene transcription by ELK1 and the STAT proteins (Seger & Krebs, 1995). The MAPK pathway was shown to be constitutively activated in a large number of AML cells, suggesting a pivotal role for this cascade in leukemogenesis (Kim et al., 1999; Towatari et al., 1997). N-Ras, but also K-Ras or H-Ras, are frequently mutated in AML cells causing dysregulation and activation of the signaling system (Bartram et al., 1989; Farr et al., 1988). As described above, altered signaling emanating from FLT3 receptors containing ITDs also relies, at least in part, on activation of MAPKs, thereby inducing autonomous growth of myeloid cell lines and primary AML blasts (Hayakawa et al., 2000). Moreover, the BCR-ABL chimeric oncoprotein that results from chromosomal translocation is yet another trigger for alterations in the MAPK pathway (Pendergast et al., 1993).

PD98059 and PD184352 are small molecule inhibitors that strongly reduce MAPK activity and profoundly impair growth and survival of AML cells (Milella et al., 2002). The primary effect of the inhibitors included cell cycle arrest followed by apoptosis in a significant percentage of leukemic blasts (Lunghi et al., 2003). The inhibitors abrogated the clonogenic properties of primary AML cells, but had only minimal effects on normal hematopoietic progenitors. Moreover, impairment of MAPK signaling sensitized leukemic cells to spontaneous, as well as drug-induced apoptosis (Milella et al., 2002; Wu et al., 2004). U0126, another potent MEK inhibitor, led to a highly significant induction of apoptosis in some AML cell lines and blasts, while no apparent responses were seen in others (James et al., 2003). Interestingly, a particularly pronounced effect on the most primitive types of leukemia, which are often found to be the most resistant to standard chemotherapy, was observed. A possible synergistic effect in combination with the chemotherapeutic agent Ara-C was also observed. Moreover, control cells were completely insensitive to the inhibitor (James et al., 2003). A phase I clinical trial addressed the question of efficacy of Sorafenib (BAY43-9006), a Raf-1 kinase inhibitor, in AML patients (Tong et al., 2006). Although no significant inhibition of the MAPK cascade, as assessed by phosphorylation of Erk, could be detected, c-Kit-mediated pathway activation was largely abolished upon treatment with the inhibitor. In fact, further analysis revealed an almost complete inhibition of c-Kit activity at high doses of the inhibitor, putting c-Kit forward as another target of Sorafenib (Tong et al., 2006).

Another approach to target the MAPK pathway is based on interfering with Ras protein function. Proper membrane localization of Ras proteins is a critical step for successful signal transduction. Binding of Ras to the plasma membrane, which is required for its full biological activity, is accomplished by diverse post-translational modifications of the protein, which are catalyzed by specific enzymes. Various inhibitors against these enzymes have been generated in order to impair the post-translational modification steps. The most significant progress has been made in the identification and characterization of farnesyltransferase inhibitors (FTIs). Treatment of tumor cells with these inhibitors results in various effects including alteration of cell cycle progression, induction of apoptosis, changes in cell morphology and inhibition of anchorage-independent growth (Sebti & Hamilton, 2000). Several FTIs have entered clinical trials for AML with promising results. Zarnestra (R115777) significantly inhibited the colony growth of human AML blasts and induced apoptosis. In combination with other drugs the effect of the FTI was even more pronounced (Korycka et al., 2004). Phase I and II clinical trials have described a promising biological activity of Zarnestra, inducing antileukemic responses in a subgroup of patients treated with the inhibitor (Karp et al., 2001; Lancet et al., 2006). Accordingly, evaluation of the FTI BMS-214662 showed strong evidence of antileukemic activity and a good tolerability of the compound in a cohort of patients with relapsed or refractory disease (Cortes et al., 2005).

3. RESULTS

3.1. Aims

Part I – Autocrine insulin-like growth factor-I signaling promotes growth and survival of human acute myeloid leukemia cells via the phosphoinositide 3-kinase/Akt pathway

RTKs and signaling cascades such as the PI3K/Akt pathway have been shown to play a crucial role in various human cancers. Promising new cancer therapies focus on pharmacological inhibitors selectively targeting signaling molecules of those survival pathways. Therefore, the role of RTK signaling and its biological function was investigated in AML. A panel of AML cell lines and patient blast cells were analyzed for the expression of various signaling proteins and their role in cellular responses. The main focus was laid on the IGF-I signaling network as high expression levels of the IGF-IR, the IR, as well as autocrine production of IGF-I were detected in the cells studied. Various approaches were aimed at investigating the potential of targeting this signaling system including RNAi, neutralizing antibodies as well as the use of the novel IGF-IR kinase inhibitor NVP-AEW541 (Novartis) as an antitumor agent in AML. Besides, the involvement of downstream transducers of the IGF-IR on AML cell growth and survival was evaluated. Class I_A PI3K isoforms were specifically targeted in order to better understand their role in cellular responses and to investigate their potential as molecular targets for cancer treatment.

Together, we could describe a novel role for autocrine IGF-I signaling in the growth and survival of AML cells. The inhibition of the IGF-IR/PI3K signaling network in combination with chemotherapeutic agents may represent a novel approach to target human AML.

Part II – Targeting PI3KC2 impairs proliferation and survival in acute leukemia, brain tumours and neuroendocrine tumours

Eight mammalian PI3K isoforms exist which are subdivided into three classes. While much attention has been given to the class I isoforms, little is known about the role of class II PI3Ks in

human cancer. Therefore, the expression pattern and functions of the class II PI3K isoform PI3KC2 β were investigated in tumor samples and cell lines from AML, glioblastoma multiforme (GBM), medulloblastoma (MB), neuroblastoma (NB), and small cell lung cancer (SCLC). Furthermore, the use of two novel isoform-specific pharmacological inhibitors (PI701, PI702) and RNAi to inhibit PI3KC2 β was evaluated. The effect on signal transduction, cell growth and survival and the potential of PI3KC2 β as a novel drug target in AML, brain tumors and neuroendocrine tumors was analyzed.

In summary, we could show that PI3KC2 β contributes to proliferation and survival of AML, brain tumors and neuroendocrine tumors and plays an important role in the migratory capacity of highly motile breast cancer cells. Moreover, inhibition of this class II PI3K isoform sensitized AML and glioblastoma cells to chemotherapeutic agent.

Part III – Investigation of the molecular determinants of rapamycin sensitivity in acute myeloid leukemia cells

Protein expression analysis in a panel of AML cells revealed significant differences in the expression levels of mTOR. Therefore, the role of mTOR in AML cell growth and survival was investigated and cellular responses to the mTOR inhibitor rapamycin were compared in cells expressing high levels of mTOR (mTOR^{high}) and cells expressing low levels of mTOR (mTOR^{low}). Moreover, an RNAi screen was aimed at uncovering kinases which modulate the sensitivity to rapamycin. Screening a kinome siRNA library identified human kinases which strongly enhanced the anti-proliferative effect of rapamycin in AML cells and played a role in tumor cell survival. The use of specific inhibitors or shRNA targeting those kinases was further aimed at investigating their potential as molecular targets for AML treatment in combination with rapamycin.

Together, our data show an important role of mTOR for cancer cell proliferation and survival in a subclass of human AML cells. Preliminary results suggest that targeting certain RTKs (IGF-IR, FLT3, FGFR1) or signal transducers (SYK, ZAP70) in combination with rapamycin bears great potential for AML therapy.

Part IV – Novel role for insulin as an autocrine growth factor for malignant brain tumour cells

Atypical teratoid/rhabdoid tumors (AT/RTs) of the central nervous system (CNS) are childhood malignancies associated with poor prognosis. To gain better insight into the molecular background of this disease, the role of RTKs and their involvement in tumor growth and survival was investigated in a panel of AT/RT and malignant rhabdoid tumor (MRT) cell lines. Overexpression of the IR and IGF-IR was detected in the cancer cells when compared to control normal brain tissue and insulin was shown to be secreted by AT/RT cells. Therefore, the potential of targeting the IR or IGF-IR signaling system in human AT/RT and MRT cell lines was investigated by the use of RNAi, neutralizing antibodies or NVP-AEW541. Several signaling proteins such as the receptors (IR and IGF-IR) as well as downstream transducers such as the class I PI3K isoform p110 α were analyzed for their impact in tumor growth and survival and their potential as anti-proliferative target.

In short, a novel role for autocrine signaling by insulin and the IR in growth and survival of malignant human CNS tumor cells could be described.

Part V – Targeting the phosphoinositide 3-kinase isoform p110 impairs growth and survival in neuroblastoma cells

Neuroblastoma (NB) is the most common extra cranial solid tumor occurring in children. Treatment outcome is still unsatisfying and a better understanding of the biology of this cancer is aimed at the identification of novel therapeutic targets in this cancer. A promising field of investigation is to target RTKs and their downstream mediators. Therefore, the role of RTK/PI3K signaling and the potential of targeting specific class I PI3K isoforms as a novel anti-proliferative approach was investigated in NB cells. Expression levels of PI3Ks was evaluated in primary human neuroblastoma samples and cell lines and the effects on cell survival and signal transduction was analyzed following isoform-specific down-regulation of p110 α or p110 δ in SH-SY5Y and LA-N-1 cells.

In conclusion, a novel function of the class I_A PI3K isoform p110 δ in neuroblastoma growth and survival was uncovered.

3.2. Autocrine insulin-like growth factor-I signaling promotes growth and survival of human acute myeloid leukemia cells via the phosphoinositide 3-kinase/Akt pathway

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ORIGINAL ARTICLE

Autocrine insulin-like growth factor-I signaling promotes growth and survival of human acute myeloid leukemia cells via the phosphoinositide 3-kinase/Akt pathway

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Insulin-like growth factor (IGF) signaling plays an important role in various human cancers. Therefore, the role of insulin-like growth factor I (IGF-I) signaling in growth and survival of acute myeloid leukemia (AML) cells was investigated. Expression of the IGF-I receptor (IGF-IR) and its ligand IGF-I were detected in a panel of human AML blasts and cell lines. IGF-I and insulin promoted the growth of human AML blasts *in vitro* and activated the phosphoinositide 3-kinase (PI3K)/Akt and the extracellular signal-regulated kinase (Erk) pathways. IGF-I-stimulated growth of AML blasts was blocked by an inhibitor of the PI3K/Akt pathway. Moreover, downregulation of the class Ia PI3K isoforms p110 β and p110 δ by RNA interference impaired IGF-I-stimulated Akt activation, cell growth and survival in AML cells. Proliferation of a panel of AML cell lines and blasts isolated from patients with AML was inhibited by the IGF-IR kinase inhibitor NVP-AEW541 or by an IGF-IR neutralizing antibody. In addition to its antiproliferative effects, NVP-AEW541 sensitized primary AML blasts and cell lines to etoposide-induced apoptosis. Together, our data describe a novel role for autocrine IGF-I signaling in the growth and survival of primary AML cells. IGF-IR inhibitors in combination with chemotherapeutic agents may represent a novel approach to target human AML.

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Introduction

Acute myeloid leukemia (AML) accounts for approximately 70–80% of acute leukemia in adults. Treatment and outcome of the disease depend on several factors, including leukemia karyotype, molecular alteration and patient age. The 5-year survival rate ranges from 65 to 15%, drastically decreasing with the age at diagnosis. Chromosomal translocations frequently result in dysfunction of transcription factors needed for normal hematopoietic development. Additional mutations have been described in the receptor tyrosine kinases FLT3, c-Kit and c-Fms, as well as in N- and K-Ras.^{1,2} The manifestation of AML is a combination of mutations conferring proliferative advantage, impaired differentiation and apoptosis.

Polypeptide growth factors have been shown to play a key role in AML proliferation and survival.^{3–5} Human AML cells express a variety of growth factor and cytokine receptors that

can be activated by mutation, overexpression and/or establishment of autocrine loops. Among these receptors are the polypeptide growth factor receptors FLT3, c-Kit, c-Fms, vascular endothelial growth factor receptor and fibroblast growth factor receptor.^{3–8} Several potential anti-AML therapeutic approaches involving the FLT3 system have been reported.^{9–11}

Insulin-like growth factor (IGF) signaling plays a major role in various human malignancies, including breast, colon and prostate cancer.¹² In leukemia, IGF signaling has not yet been extensively studied, although expression of the IGF-I receptor (IGF-IR) was reported in human AML cells.^{13,14} Autocrine IGF-I production has been suggested to play a role in drug resistance in an AML cell line.¹⁵ In addition, IGF-I signaling has a crucial function in other hematological malignancies such as multiple myeloma,¹⁶ and several anti-IGF-IR experimental therapies were shown to inhibit multiple myeloma proliferation *in vitro* and *in vivo*.¹⁷

A critical intracellular signaling mediator of the IGF-IR is the phosphoinositide 3-kinase (PI3K)/Akt pathway.^{18,19} Indeed, PI3K signaling is implicated in the control of cell proliferation, survival and motility/metastasis downstream of many different growth factor receptors.²⁰ The importance of PI3K signaling in human cancer is highlighted by the fact that mutations in the tumor suppressor gene *PTEN* occur frequently in human tumors.^{20,21} *PTEN* is a phosphatase that antagonizes the action of PI3K by dephosphorylating the D-3 position of polyphosphoinositides.²² Moreover, recent reports have described activating mutations in the *PIK3CA* gene encoding the catalytic p110 α isoform of class Ia PI3K in a variety of human cancers, including, breast, colon and ovarian cancer.^{23,24} Mutations in the *PTEN* gene have not been found in a high percentage of AML cases, although they were documented in AML cell lines.^{21,25} Moreover, a recent screen comprising AML cases did not reveal any mutations in the gene encoding p110 α ,²⁶ suggesting a possible deregulation of other class Ia PI3Ks, namely p110 β and p110 δ in hematological malignancies. In support of this notion, constitutive activation of Akt/PKB has been reported by several studies in human AML blasts.^{27,28} In the context of leukemia, altered PI3K signaling was also shown to play a role in the development of adult T-cell lymphoma.²⁹

In the present report, we have investigated the expression pattern and biological functions of components of the IGF-IR signaling system in human AML blasts and cell lines. Moreover, we have evaluated the potential of the novel IGF-IR kinase inhibitor NVP-AEW541³⁰ as an antitumor agent in AML. Finally, we have investigated whether targeting downstream signaling mediators of the IGF-IR could suppress growth and induce apoptosis in AML cell lines. Our findings describe for the first time a role for autocrine signaling by IGF-I and the IGF-IR in growth, survival and chemoresistance of AML cells, which involves the PI3K/Akt pathway.

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Materials and methods

Reagents and antibodies

Antibodies and reagents were purchased from the following companies: IGF-IR β , IR β , p85 α , p110 β , p110 δ , PTEN, Akt/PKB, Erk1/2, PARP, IGF-I and p-Tyr (Santa Cruz Biotechnology, Santa Cruz, CA, USA); p110 α (clone U3A) (generous gift from Dr A Klippel); 16F-11 (Novus Biologicals, Littleton, CO, USA); actin, insulin (Sigma-Aldrich, St Louis, MO, USA); activated Akt/PKB (Ser473, Thr308), activated Erk1/2 (Thr202/Tyr204) (Cell Signaling Technology, Danvers, MA, USA); LY294002, IGF-I, IGF-IR neutralizing antibody (Calbiochem, La Jolla, CA, USA); IR neutralizing antibody (Biosource, Camarillo, CA, USA); siGENOME siRNA (Dharmacon, Lafayette, CO, USA); NVP-AEW541 (Novartis Pharma AG, Basel, Switzerland); TGX-221 (Prof. SP Jackson, Camarillo, CA, USA); IC87114 (ICOS Corporation, Indianapolis, IN, USA).

Cell culture

Human AML cell lines were grown in RPMI (Life Technologies Invitrogen, Carlsbad, CA, USA) with 10% (v/v) fetal calf serum (FCS) and penicillin/streptomycin/L-glutamine and passaged every 3–5 days by dilution. For growth factor stimulations, cells were incubated overnight in Optimum medium (Life Technologies/Invitrogen) and washed with serum-free medium before incubation with growth factors. Immortalized B cells³¹ were cultured in RPMI with 20% (v/v) FCS and penicillin/streptomycin/L-glutamine. Heparinized peripheral blood or bone marrow samples were obtained from adult patients with AML. Each sample contained more than 90% blast cells. AML diagnosis was based on the criteria of the French–American–British Cooperative Group and immunophenotypic studies. Blast cells, isolated by centrifugation on Ficoll–Hypaque, were used immediately or kept frozen until use. Cell viability, as assessed by Trypan blue exclusion, was greater than 80% after 4–12 h of blast cell culture in RPMI medium/10% FCS. Immunophenotypic analysis was performed using a large panel of directly fluorescein isothiocyanate (FITC)- or phycoerythrin-conjugated mAbs reacting with leukocyte differentiation antigens CD-2, -3, -4, -7, -10, -13, -14, -15, -19, -20, -22, -33, -34, -41, -61, glycoporphin A, HLA-DR, TdT or myeloperoxidase (antibodies were from Becton Dickinson, Franklin Lake, NJ, USA; Immunotech-Coulter, Miami, FL, USA; DAKO, Troy, MI, USA). Unconjugated mAbs were detected by indirect immunofluorescence using an FITC-conjugated goat anti-mouse antibody (Fab92 fragment; Tago). Double-immunofluorescence analysis was performed with an Epics flow cytometer (Coulter Electronics, Fullerton, CA, USA).

RT-PCR analysis

RNA was isolated using the RNeasy Mini Kit (Qiagen, Santa Cruz, CA, USA) from 1×10^6 cells. Reverse transcription-polymerase chain reaction (RT-PCR) was performed according to the QIAGEN OneStep RT-PCR protocol. Expression of IGF-1R, IR, IGF-I, IGF-II and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was analyzed using the following primers: IGF-IR-FP, 5'-ACTTCTGCGCCAACATCCTCA-3'; IGF-IR-RP, 5'-GGGAAATCAGGGGCGAGTGAAGG-3'; IR-FP, 5'-GCTGAAGCTGCCCTCGAGGA-3'; IR-RP, 5'-CGGCCACCGTCACATTCCA-3'; IGF-I-FP, 5'-GTGCTGCTTTTGTGATTCTT-3'; IGF-I-RP, 5'-GTC TTGGGCATGTCGGTGTGG-3'; IGF-II-FP, 5'-ATGGGGAAGTC GATGCTGGTG-3'; IGF-II-RP, 5'-ACGGGGTATCTGGGAAG TTG-3'; GAPDH-FP, 5'-AACGTGTCTAGTGGTGACCT-3'; GAP DH-RP, 5'-GGGTGTCGCTGTTGAAGTCA-3'.

ELISA assays

Enzyme-linked immunosorbent assay (ELISA) was performed on cell culture supernatant of AML blasts or cell lines kept in culture for 3 days. A fully serum-free culture system of RPMI containing bovine serum albumin (15 mg/ml), cholesterol (7.8 μ g/ml) and transferrin (7.7 μ M) was used for AML cell proliferation. Ninety-six-well plates (Costar EIA/RIA 96-well plates; Corning Incorporated, Corning, NY, USA) were coated with 100 μ l of the supernatant, and antibodies specific for IGF-I or IGF-II were used to detect the presence of IGF-I and IGF-II, respectively. Horseradish peroxidase-conjugated donkey anti-rabbit IgG (Amersham Biosciences, Buckinghamshire, UK) was subsequently used for detection by addition of tetramethylbenzidine-H₂O₂ (TMB peroxidase EIA substrate kit; Bio-Rad Laboratories, Hercules, CA, USA), and the absorbance was measured according to the manufacturer's protocol.

Cell proliferation

AML cell lines (5×10^3 cells/well) were seeded in 96-well plates and grown for 72 h in serum (10%)-containing medium in the presence or absence of inhibitors. For growth factor stimulations, cells were incubated in Optimum medium (Life Technologies/Invitrogen). The number of viable cells was analyzed by means of an MTS assay using the CellTiter 96 Aqueous One Solution Cell Proliferation Assay (Promega, Madison, WI, USA), according to the manufacturer's instructions. Data are mean with s.d. from eight repetitions.

Apoptosis

For detection of apoptosis, AML cells were incubated for 16–24 h in the presence or absence of inhibitors and analyzed for caspase-3 and -7 activity using the Caspase-Glo 3/7 Assay (Promega) according to the manufacturer's instructions. Alternatively, the cells were lysed and caspase-3 activity was measured using the CasPACE Assay System (Promega). Additionally, samples were analyzed by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and western blot with anti-poly(ADP-ribose) polymerase (PARP) antibodies.

Transient and stable expression in AML cells

U937 cells were transfected with small interfering RNA (siRNA) targeting the IGF-IR or IR and small hairpin RNA (shRNA) constructs³² targeting or the parental pRetroSuper vector p110 β (PIK3CB) or p110 δ (PIK3CD) using the Amaxa Nucleofector system (Amaxa biosystems, Gaithersburg, MD, USA) according to the manufacturer's protocol. Cell Line Nucleofector Kit V was used and program V-001 applied. Constructs were from the library described previously.³² After 48 and 72 h of transfection, cells were analyzed for cell proliferation by an MTS assay and lysed in cell lysis buffer in order to visualize protein expression by SDS-PAGE and western blotting. Alternatively, transfected cells were resuspended in fresh medium containing puromycin at 2 μ g/ml and selected for 3–4 weeks. Puromycin-resistant U937 cells were maintained in media containing 2 μ g/ml puromycin as stable transfectants.

SDS-PAGE and western blot analysis

Cellular lysates were prepared as described previously,³³ separated by SDS-PAGE, transferred to a hydrophobic polyvinylidene difluoride membrane (Hybond-P; Amersham Biosciences), and immunoblotted with various antibodies according to the manufacturer's protocol. Chemiluminescence was used

for visualization using the enhanced chemiluminescence western blotting detection reagents (Amersham Biosciences) according to the manufacturer's protocol.

Immunoprecipitation

Cells were kept in medium without serum and stimulated with IGF-I or insulin for 10 min at 37°C. The cells were then lysed in lysis buffer (1% Triton X-100) and incubated with Protein G-Sepharose beads (GE Healthcare, Piscataway, NJ, USA) and α -p-Tyr antibody for 3 h at 4°C with mixing. After washing with cold lysis buffer, samples were denatured in SDS-PAGE loading buffer and analyzed by western blot.

Colony-forming assay

Bone marrow CD34⁺ cells (Lonza, Basel, Switzerland) were cultured at different densities (200, 500, 1000 per ml) in 1 ml human methylcellulose complete media (HSC004; R&D Systems, Minneapolis, MN, USA) with increasing concentrations of NVP-AEW541. Each condition was evaluated twice in duplicates. Colonies, defined as aggregates >50 cells, were scored after 14 days incubation at 37°C in a fully humidified atmosphere with 5% CO₂.

Results

Characterization of the expression of the IGF-IR, IGFs and signaling intermediates in a panel of human AML blasts and cell lines

In view of the crucial role of IGF-I signaling in a variety of human cancers, we have studied the expression and biological functions of components of the IGF-IR pathway in human AML cells. A panel of 20 primary human AML blasts (Supplementary Table 1) and 7 low passage AML cell lines was analyzed for the expression of the IGF-IR and insulin receptor (IR) by western blot and RT-PCR analysis of cell lysates. The IR was studied in parallel with the IGF-IR, since the response of cancer cells to anti-IGF-IR inhibitors may also be modulated by expression of the related IR. Nonleukemic human bone marrow cells were used as a normal control for the western blot analysis. Moderate to high IGF-IR β expression levels were found in 16/20 of the blasts and in all the cell lines (Figure 1a and Supplementary Figure 1a). The IR was expressed in 19/20 blasts with overexpression in 17 of the 19 cases, as compared to nonleukemic bone marrow cells, and in cell lines such as U937 and THP1. Expression analysis of class I α PI3K isoforms revealed a consistent overexpression of the regulatory subunit p85 α in AML blasts and cell lines, while expression of the catalytic p110 α subunit was restricted to a small number of blasts and the KG-1 cell line (Supplementary Figures 1a and b). Consistently, RT-PCR analysis revealed only low mRNA levels of this isoform in AML cell lines (data not shown). In contrast, the class I α PI3K catalytic isoforms p110 β and p110 δ displayed a broader expression pattern in AML blasts and cell lines, and overexpression was found in more than 50% of the blasts. The western blot analysis revealed no significant differences in expression of the downstream signaling intermediate extracellular signal-regulated kinase (Erk) (Supplementary Figure 1c), while Akt/PKB levels were elevated in the AML blasts, when compared to nonleukemic bone marrow cells. Constitutive activation of Akt/PKB was detected in all AML blasts and cell lines, while some of the blasts and cell lines also displayed detectable activation of Erk1/2.

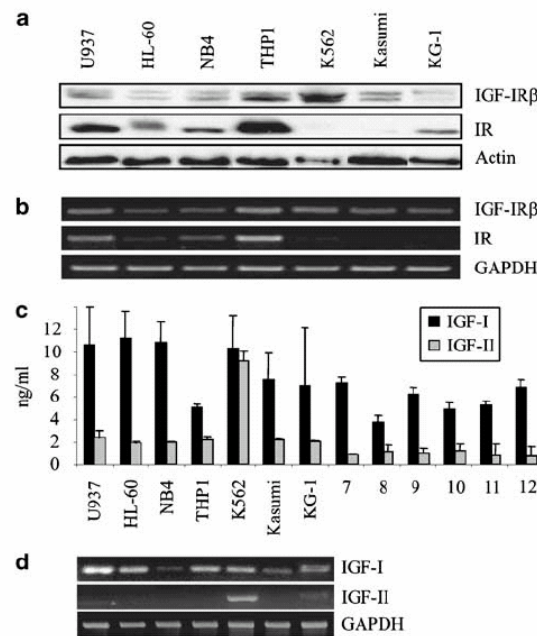


Figure 1 Expression of the insulin-like growth factor I receptor (IGF-IR), insulin receptor (IR) and insulin-like growth factors (IGFs) in human AML patient blasts and cell lines. (a) Equal amounts of lysates from seven AML cell lines (U937, HL-60, NB4, THP1, K562, Kasumi, KG-1) were analyzed by western blotting with antibodies specific for the indicated proteins. Actin was used as a loading control. (b) Analysis of IGF-IR and IR mRNA levels by RT-PCR in leukemic cell lines. Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was analyzed as a control. (c) Measurement of IGF-I and IGF-II secretion in the medium by leukemic cell lines and patient blasts (7–12; FAB M1, M2, M4, M5) by ELISA. Supernatant of cells kept in serum-free medium for 72 h was analyzed using antibodies specific for IGF-I and IGF-II. The background absorbance of the cell culture medium was subtracted from each sample. (d) Analysis of IGF-I and IGF-II mRNA levels in leukemic cell lines by RT-PCR.

The expression of the ligands of the IGF-IR was then investigated in the AML blasts and cell lines by RT-PCR and ELISA. AML cell lines grown under serum-free conditions secreted detectable levels of IGF-I into the culture medium, as assessed by ELISA (Figure 1c), which correlated with RT-PCR analysis revealing broad expression of the IGF-I mRNA in most of the AML cell lines (Figure 1d). In contrast, IGF-II expression was restricted to the K562 cell line. The levels of IGF-I and IGF-II secreted in the supernatant of AML cell lines were in the range of 6–12 and 10 ng/ml, respectively. At these concentrations, IGF-I was able to activate downstream signaling events (Figure 2c), implying that the amounts of IGF-I secreted by AML cells are biologically relevant. IGF-I secretion was also detected in primary AML blasts, confirming the results obtained in cell lines (Figure 1c). Thus, primary AML blasts and cell lines expressing the IGF-IR, IR, the ligand IGF-I and downstream signaling mediators such as class I α PI3K isoforms.

IGF-I and insulin promote growth of AML blasts through the PI3K pathway

The ability of IGF-I and insulin to promote growth of human AML blasts *in vitro* was then investigated. Treatment of isolated

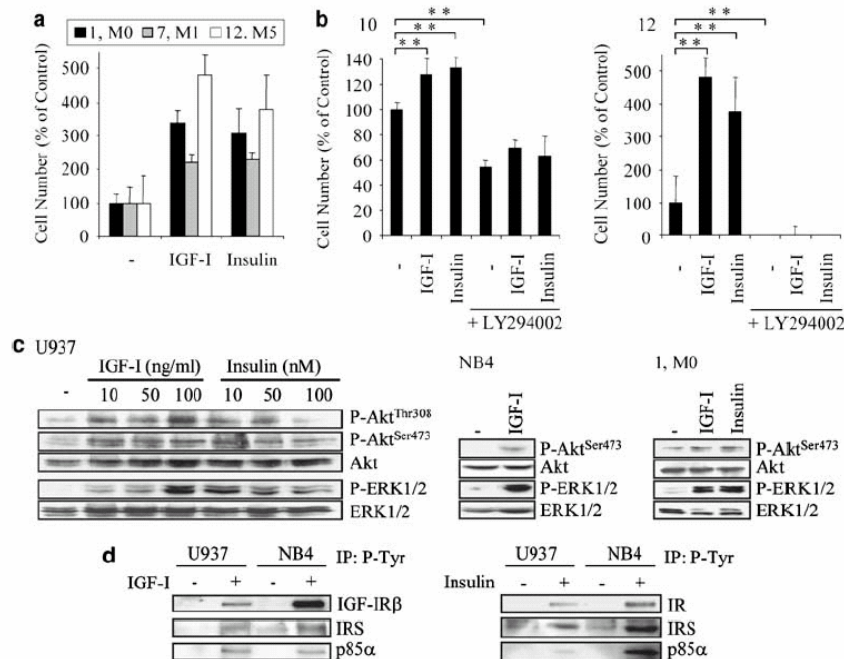


Figure 2 Insulin-like growth factor I (IGF-I) and insulin stimulate proliferation of AML cells through activation of the PI3K/Akt pathway. (a) Cell proliferation of AML patient blasts by stimulation with IGF-I (25 ng/ml) or insulin (50 ng/ml). (b) Inhibition of IGF-I- or insulin-stimulated AML cell proliferation by the PI3K inhibitor LY294002 (10 μ M) in AML patient blasts. * $P < 0.05$ or ** $P < 0.01$ by analysis of variance test. (c) Serum-starved U937, NB4 or primary blasts were stimulated with different concentrations of IGF-I or insulin for 10 min and evaluated by western blotting for the phosphorylation status of Akt/PKB (Thr308; Ser473) and Erk1/2 (Thr202/Tyr204). (d) Anti-phosphotyrosine immunoprecipitation (P-Tyr) from IGF-I- or insulin-stimulated U937 and NB4 cells. Cell lysates were analyzed by western blotting for IGF-IR, insulin receptor (IR), insulin receptor substrate (IRS) and p85 α .

blasts with IGF-I or insulin resulted in a two- to fourfold increase in AML blast growth after 48 h in serum-containing medium (Figure 2a). The optimal concentrations of IGF-I and insulin for promotion of blast growth were 25 and 50 ng/ml, respectively. These results were observed in a panel of human AML blasts including AML M0, M1 and M5. To investigate whether the PI3K pathway was involved in the growth-promoting effects of IGF-I and insulin, AML blasts were treated with the pharmacological inhibitor LY294002 in combination with growth factors. The pharmacological inhibitor impaired IGF-I- and insulin-stimulated growth of primary AML blasts *in vitro* (Figure 2b).

The activation of the PI3K and Erk pathways by IGF-I and insulin was then investigated in AML cells by monitoring the phosphorylation status of the downstream targets Akt and Erk1/2. Optimal concentrations of IGF-I (100 ng/ml) and insulin (10–50 nM) resulted in the rapid induction of Akt phosphorylation on Thr308 and Ser473, as well as in phosphorylation of Erk1/2 in U937 cells (Figure 2c). Comparable results were also obtained in the NB4 cell line and in AML blasts. Thus, IGF-I and insulin promote AML cell growth by activating the PI3K/Akt signaling pathway. Stimulation of U937 and NB4 cells with IGF-I or insulin induced the recruitment of the receptors to phosphotyrosine-containing signaling complexes also containing the insulin receptor substrate-1 and the PI3K regulatory subunit p85 α (Figure 2d).

Downregulation of the PI3K isoforms p110 β and p110 δ impairs AML cell growth, induces apoptosis and impairs Akt activation by IGF-I

The results from the expression analysis of PI3K isoforms in AML blasts and cell lines had revealed consistent expression of the PI3K isoforms p110 β and p110 δ (Supplementary Figure 1b), indicating a possible role for these enzymes in AML cell responses. Moreover, inhibition of PI3K activity with LY294002 impaired growth of AML blasts induced by IGF-I and insulin (Figure 2b). An RNA interference (RNAi) approach was used to specifically downregulate the expression of p110 β and p110 δ in U937 cells. Western blot analysis confirmed the specific downregulation of the PI3K isoforms upon transfection with the corresponding (short hairpin) shRNA construct (Figure 3a). U937 cells stably transfected with either p110 β and p110 δ shRNA displayed reduced growth in serum-containing medium (Figure 3b). Moreover, the p110 β and p110 δ shRNA-transfected cells were more sensitive to apoptosis induced by serum withdrawal, as assessed by the induction of caspase-3 activation (Figure 3b).

Resistance of human AML cells to chemotherapy is a frequent cause of treatment failure. Therefore, we next investigated whether downregulation of p110 β or p110 δ could sensitize human AML cells to the action of chemotherapeutic agents. Treatment with cytarabine (Ara-C) or etoposide significantly enhanced the suppression of cell growth in p110 δ shRNA-

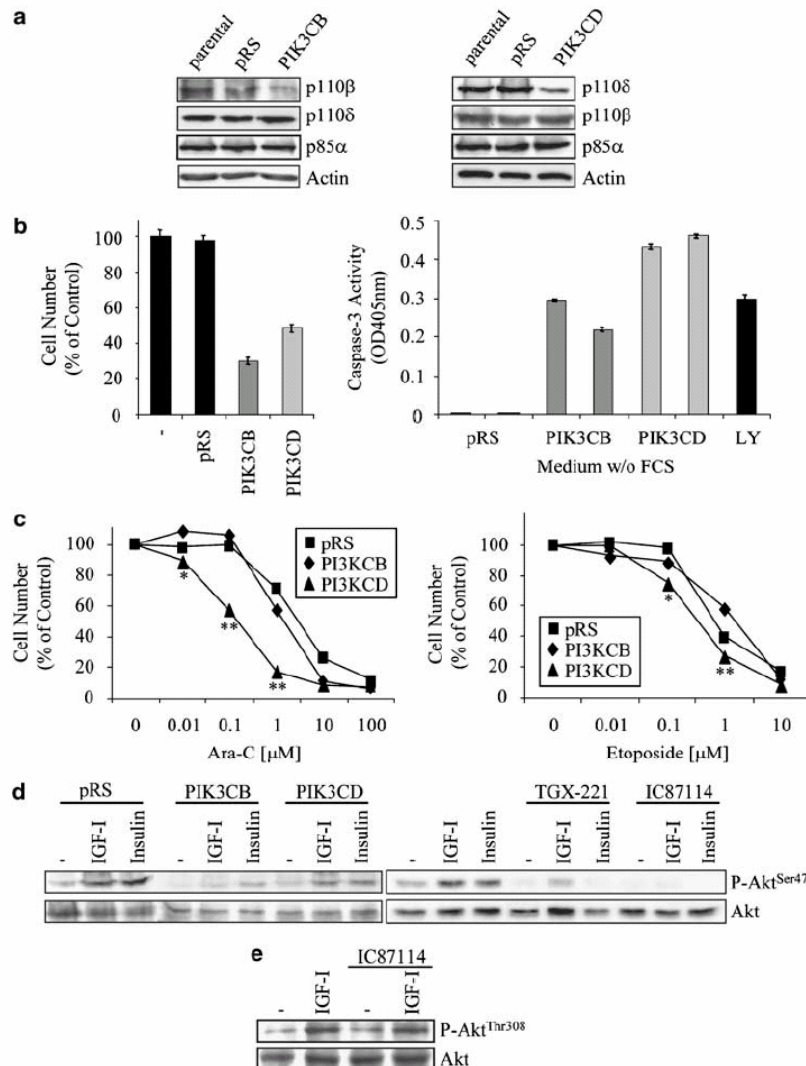


Figure 3 Downregulation of PI3K isoforms p110 β or p110 δ reduces cell viability of AML cells and sensitizes the cells to chemotherapeutic agents. (a) U937 cells were stably transfected with shRNA against the class I α PI3K isoforms p110 β (PIK3CB) or p110 δ (PIK3CD) or the empty vector (pRS) as a control. Downregulation of the protein was visualized by western blot analysis using isoform-specific antibodies. (b) U937 cells transfected with shRNA against p110 β (PIK3CB), p110 δ (PIK3CD) or the empty pRetroSuper vector were assayed for cell proliferation by MTS assay (left). Apoptosis was analyzed in serum-free medium (RPMI W/O FCS or OPTIMEM) by caspase-3 activity measurement. LY294002 (10 μ M) was used as a control (right). (c) Cell proliferation rate was analyzed in U937 cells transfected with shRNA against p110 β (PIK3CB), p110 δ (PIK3CD) or the empty pRetroSuper vector incubated with increasing concentrations of cytarabine (Ara-C) or etoposide. * P <0.05 or ** P <0.01 by analysis variance test. (d) U937 cells transfected with shRNA against p110 β (PIK3CB), p110 δ (PIK3CD) or the empty pRetroSuper vector (left) or pretreated with PI3K isoform-specific inhibitors against p110 β (TGX-221; 10 μ M) or p110 δ (IC87114; 10 μ M) (right) were kept in medium without serum, stimulated with insulin-like growth factor I (IGF-I) or insulin and analyzed by western blotting for the phosphorylation status of Akt/PKB (Ser473). (e) IC87114-treated KG-1 cells were stimulated with IGF-I and analyzed by western blotting for the phosphorylation of Akt/PKB (Thr308).

transfected cells at concentrations in the range of 0.01–1.0 μ M (Figure 3c).

To investigate whether p110 β or p110 δ transduce signals from the activated IGF-IR or IR in AML cells, activation of Akt was analyzed in shRNA-transfected cells. U937 cells transfected with shRNA targeting p110 β and p110 δ displayed impaired activation of Akt in response to IGF-I or insulin (Figure 3d). To confirm these

findings, a pharmacological approach using isoform-specific p110 β or p110 δ inhibitors was also used in U937 cells. The p110 β -specific inhibitor TGX-221³⁴ and the p110 δ -specific inhibitor IC87114³⁵ effectively impaired activation of Akt by IGF-I or insulin (Figure 3d). IC87114 did not affect IGF-I-stimulated Akt phosphorylation in KG-1 cells expressing very low levels of p110 δ (Figure 3e), confirming the selectivity of the inhibitor.



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Together these data show that the class I_A PI3K isoforms p110 β and p110 δ play a major role in AML cell growth and survival. In addition, p110 δ appears to play a selective role in chemoresistance in AML cells. Moreover, p110 β and p110 δ transduce signals from the activated IGF-IR leading to Akt activation in AML cells.

Pharmacological inhibitors of the IGF-IR or neutralizing antibodies impair AML cell growth and induce apoptosis

The ability of the specific IGF-IR kinase inhibitor NVP-AEW541³⁰ to block AML cell growth in serum-containing medium was then investigated. NVP-AEW541 potently suppressed growth of NB4 and Kasumi cells (IC₅₀ = 0.7 and 0.4 μ M)

after 72 h, but was less efficient at inhibiting growth of HL-60 (IC₅₀ = 6.3 μ M), U937 (IC₅₀ = 7.6 μ M) and THP1 (IC₅₀ = 9.7 μ M) (Figures 4a and b). The inhibitor was also able to suppress growth of AML blasts isolated from patients (Figure 4a) with IC₅₀ values in the range of 2.2–13 μ M. Nonleukemic bone marrow cells or immortalized B cells were comparatively resistant to NVP-AEW541. The expression levels of the IGF-IR β , which is the target of NVP-AEW541, did not correlate with the sensitivities of the AML cell lines to the inhibitor (Figures 1a and 4a). The highest levels of IR expression were found in some of the cell lines with reduced sensitivity to the inhibitor such as U937 and THP1. In order to rule out potential cytotoxic effects of NVP-AEW541 on normal hematopoiesis, the inhibitor was tested at different concentrations on CD34⁺ hematopoietic progenitors from a healthy donor. Whereas high concentrations

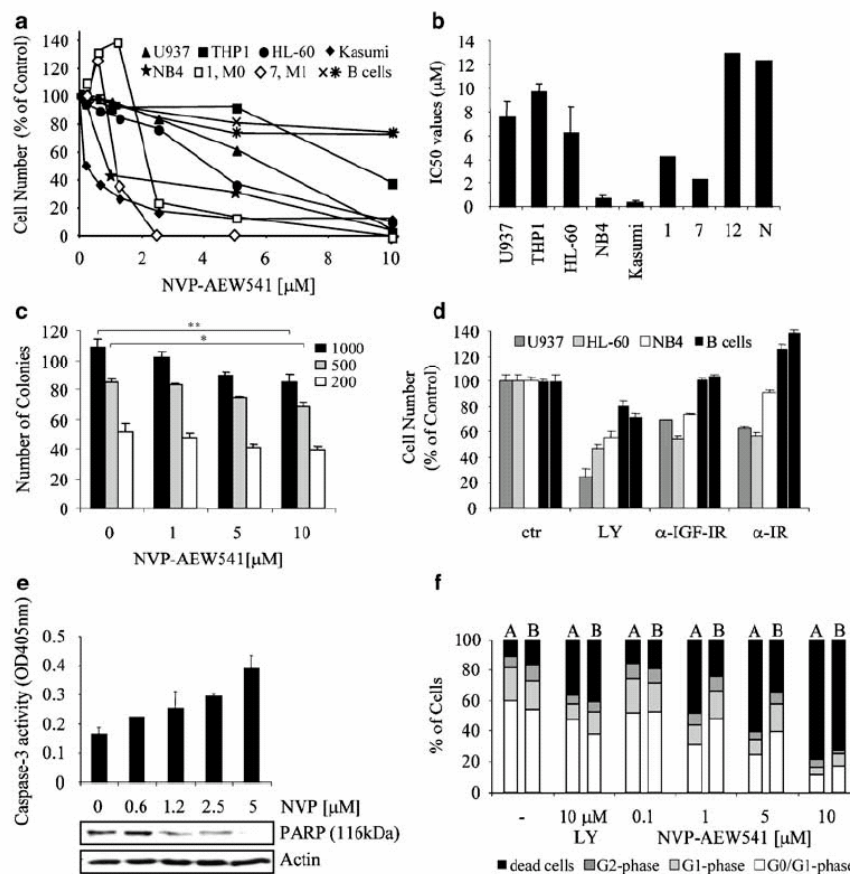


Figure 4 Inhibition of AML cell proliferation and induction of apoptosis by an insulin-like growth factor I receptor (IGF-IR) kinase inhibitor or an anti-IGF-IR neutralizing antibody. (a) Cell proliferation rate analyzed by MTS assay in AML cell lines, patient blasts and immortalized B cells incubated with increasing concentration of NVP-AEW541. (b) Sensitivity of AML cell lines, patient blasts and Ficoll-purified normal bone marrow cells (N) to the IGF-IR kinase inhibitor NVP-AEW541 by evaluation of the IC₅₀ values from proliferation assays. (c) Colony growth of NVP-AEW541 treated CD34⁺ hematopoietic progenitor cells in semisolid growth medium. Cells were plated at different densities (200, 500, 1000 cells in 1 ml medium), treated with increasing concentrations of the inhibitor (1, 5, 10 μ M) and analyzed after 14 days incubation. * P < 0.05 or ** P < 0.01 by analysis of variance test. (d) U937, HL-60, NB4 cells and immortalized B cells were treated with anti-IGF-IR (1 μ g/ml) or anti-IR (5 μ g/ml) neutralizing antibodies and proliferation was measured by MTS assay. Cell proliferation rate was expressed as percentage of cells treated with a control antibody (CTR, OKT3). LY294002 was used as a control. (e) AML patient blasts (1; FAB M0) were incubated with increasing concentrations of NVP-AEW541 and analyzed for caspase-3 activity and PARP cleavage. The band corresponding to uncleaved PARP (116 kDa) is shown. (f) NB4 (A) and U937 (B) cells were incubated with increasing concentrations of NVP-AEW541 and DNA fragmentation was analyzed by detection of cells with fractional (Sub-G₁) DNA content using propidium iodide (PI) staining and FACS analysis.

(10 μ M) significantly decreased the colony-forming ability (20% reduction), low concentrations (1–5 μ M) of the inhibitor did not significantly affect the response (Figure 4c).

To confirm the data obtained with the IGF-IR kinase inhibitor, a neutralizing antibody directed against the receptor was tested for its ability to inhibit AML cell proliferation. Three AML cell lines (U937, HL-60 and NB4) were analyzed. A significant inhibition of cell proliferation was observed when all three AML cell lines were treated with the IGF-IR neutralizing antibody, as compared to a control (OKT3) antibody or immortalized B cells (Figure 4d). Similar results were obtained with a neutralizing antibody against the IR in U937 and HL-60 cells, but not in NB4, which express low levels of the receptor (Figure 1a).

The ability of the IGF-IR kinase inhibitor to induce apoptosis was then investigated in AML blasts and cell lines. Treatment of purified AML blasts with increasing concentrations of NVP-AEW541 resulted in increased activation of caspase-3 and enhanced cleavage of PARP (Figure 4e), demonstrating the induction of apoptosis in these cells. Consistently, NVP-AEW541-induced cell death was observed in NB4 and U937 cells, as assessed by propidium iodide (PI) staining and fluorescence-activated cell sorting analysis (Figure 4f). Reduced cell proliferation was also observed when U937 cells were transfected with siRNA specifically targeting the IGF-IR or IR (Figures 5a and b), further confirming the results obtained with NVP-AEW541 or neutralizing antibodies.

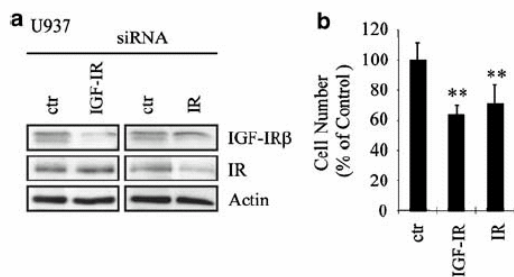


Figure 5 Inhibition of AML cell proliferation by small interfering RNA (siRNA) targeting the insulin-like growth factor I (IGF-IR) or insulin receptor (IR). (a) U937 cells transfected with control siRNA or siRNA targeting the IGF-IR or the IR were analyzed by western blotting for the expression of the receptors. (b) Cell proliferation of U937 cells transfected with siRNA targeting the IGF-IR or IR was analyzed by MTS assay. ** $P < 0.01$ by analysis of variance test.

Inhibition of the IGF-IR kinase activity enhances the effects of apoptosis in AML blasts and cell lines induced by etoposide or Ara-C

AML treatment is frequently complicated by resistance to chemotherapy. On that account, we investigated whether inhibition of IGF-IR signaling by NVP-AEW541 could sensitize human AML cells to the action of chemotherapeutic agents. Increasing concentrations of etoposide or Ara-C resulted in effective suppression of cell growth in U937, THP1, HL-60 and NB4 AML cell lines with IC_{50} values in the range of 1.0–5.0 μ M and 0.1–2.0 μ M, respectively (data not shown). AML cells were then exposed to etoposide or Ara-C (1.0 μ M each) in the presence of increasing concentrations of NVP-AEW541. Combination treatment enhanced the effect of IGF-IR inhibition in NVP-AEW541-sensitive cells (Figure 6a), whereas the effect was negligible in cells with lower responsiveness to the inhibitor (Figure 6b). Already at a low concentration of etoposide (1.0 μ M), nontoxic concentrations of NVP-AEW541 increased the effect of the chemotherapeutic drug on NB4 cells

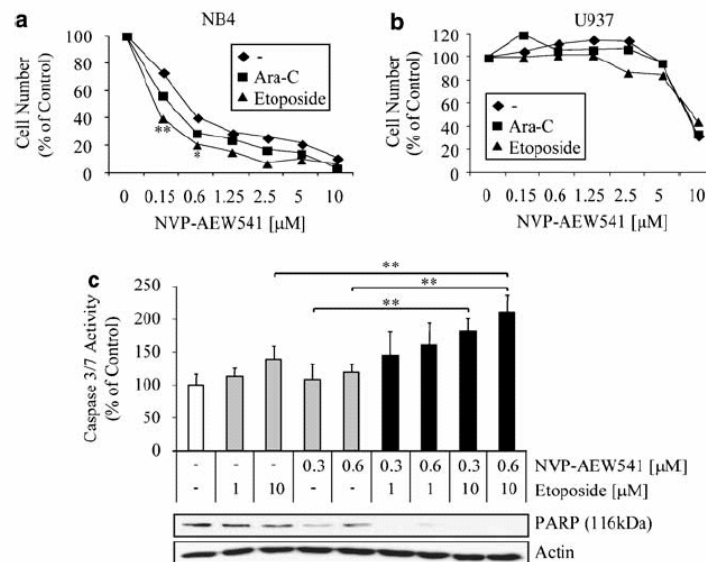


Figure 6 NVP-AEW541 sensitizes AML cells to chemotherapeutic agents. Cell proliferation rate of (a) NB4 or (b) U937 cells incubated with increasing concentrations of NVP-AEW541 in the absence or presence of cytarabine (Ara-C) or etoposide (1.0 μ M each). A representative experiment (out of three) performed with eight repetitions is shown. * $P < 0.05$ or ** $P < 0.01$ by analysis of variance test. (c) AML patient blasts (13; FAB M5) were treated with different concentrations of NVP-AEW541 (0.3, 0.6 μ M) in combination with different concentrations of etoposide (1.0, 10 μ M). Cell lysates were analyzed for caspase-3 activity and evaluated by western blotting for PARP cleavage. The band corresponding to uncleaved PARP (116kDa) is shown.



(Figure 6a). Furthermore, combination treatment of etoposide and NVP-AEW541 elevated caspase-3 activity in primary AML blasts and induced PARP cleavage (Figure 6c), demonstrating enhanced apoptosis. Thus, pharmacological IGF-IR kinase inhibitors sensitize human AML cells to etoposide.

Discussion

Pharmacological inhibitors targeting the tyrosine kinase activity of receptor tyrosine kinase (RTKs) have been extensively studied as antitumor agents, such as in the case of the epidermal growth factor receptor in solid tumors and FLT3 inhibitors in leukemia.^{9,36} Differences in the sensitivities of human tumor cells to such agents can be caused by mutations in the receptor.³⁷ Thus, in leukemia, FLT3 mutations were reported to correlate with sensitivity of tumor cells to RTK inhibitors.³⁸ Moreover, FLT3 mutations were recently shown to correlate with decreased patient survival in AML patients.³⁹ Although activating mutations have not been described in the IGF-IR in most human cancers, the receptor is frequently activated by overexpression and/or establishment of autocrine loops involving the ligands IGF-I and IGF-II.^{12,40} Previous reports have investigated the expression of the IGF-IR in human AML cells and described a role for IGF-I as a growth factor for these cells in combination with other cytokines.^{13,41} Increased serum levels of the IGFBP-2 have also been observed in patients with AML.⁴²

In the present study, we have further investigated the biological role of IGF-IR signaling in human AML blasts and cell lines. For the first time, we show that IGF-I promotes growth of AML blasts and activates intracellular signaling mediators including the PI3K/Akt and Erk pathways. Expression of the IGF-IR was found in a panel of primary AML blasts and cell lines, and IGF-I was consistently secreted by blasts and cell lines, implying that an autocrine signaling loop involving IGF-I and the IGF-IR is present in AML. Indeed, the levels of IGF-I detected in the supernatant of AML cells were shown to activate intracellular signaling events in the cells, implying that they are biologically relevant. The autocrine signaling loop involving IGF-I may contribute to the constitutive activation of Akt observed in AML blasts and cell lines. Moreover, the related IR was also found overexpressed in AML blasts, as compared to nonleukemic bone marrow cells, and insulin was able to activate PI3K/Akt and Erk in a manner comparable to IGF-I. Thus, both IGF-I and insulin may represent novel growth factors playing a crucial role in AML cell proliferation *in vivo*.

The IGF-IR kinase inhibitor NVP-AEW541 was able to reduce growth of AML blasts and cell lines, although differences in sensitivities were observed. In the case of some AML cell lines, high levels of expression of the IR were found in cells with reduced sensitivities to NVP-AEW541, which is in agreement with the observation that the inhibitor also blocks the protein tyrosine kinase activity of the IR at higher concentrations than the IGF-IR.³⁰ In support of this notion, both IGF-IR and IR neutralizing antibodies partially reduced the growth of AML cell lines. However, additional molecular mechanisms may render some AML cell lines or primary blasts resistant to IGF-IR inhibitors. Indeed, autocrine stem cell factor/c-Kit signaling was shown to reduce the sensitivity of human small cell lung cancer cells to the related IGF-IR kinase inhibitor NVP-ADW742.⁴³ Moreover, enhanced activation of Akt was also recently shown to protect human neuroblastoma cells from the effects of NVP-AEW541.³³ Finally, it was shown that, in hematopoietic cells transfected with the IGF-IR, pharmacological inhibitors of PI3K/Akt/mTOR and the Raf/MEK/Erk pathways enhanced the effects

of IGF-IR neutralizing antibodies.⁴⁴ Thus, a variety of mechanisms could explain the differences in sensitivities to NVP-AEW541 observed in AML blasts and cell lines. The ability of NVP-AEW541 to suppress the growth of AML cells was in part the result of induction of apoptosis, suggesting that the IGF-IR plays a role in survival of AML cells. The IGF-IR kinase inhibitor also sensitized AML cells to the chemotherapeutic agent etoposide, an observation that was previously made in other cancer cell lines.⁴⁵ Thus, IGF-IR signaling also plays a role in the resistance of AML cells to chemotherapeutic agents. Non-leukemic bone marrow cells, normal CD34⁺ hematopoietic progenitors and immortalized B lymphocytes were resistant to pharmacological IGF-IR inhibitors and neutralizing antibodies, indicating that targeting IGF-IR signaling may result in selective killing of AML cells, as compared to normal leukocytes *in vivo*.

PI3K signaling was demonstrated to contribute to AML cell growth and survival,⁴⁶ and recent reports showed that the class I_A PI3K isoform p110 δ plays a major role in AML cell proliferation.^{47,48} By using RNAi, we show for the first time that in addition to p110 δ , the PI3K isoform p110 β also plays a role in AML cell growth and survival. These observations were supported by the broad expression of these two isoforms in AML blasts and cell lines. Indeed, this is the first study showing that p110 β is overexpressed in most AML cases. The overexpression of p110 δ in AML blasts and cell lines investigated here is consistent with previous studies.^{47,48} In contrast, only low levels of p110 α mRNA and protein could be found in the subset of patient samples and AML cell lines analyzed in this study. These differences could be caused by the heterogeneity and relatively small size of the samples analyzed in each study. Interestingly, RNAi or pharmacological inhibitors targeting p110 β and p110 δ reduced Akt activation by IGF-I or insulin, implying that both PI3K isoforms can couple to the activated IGF-IR or IR in AML cells. Recent reports have demonstrated a selective role for p110 α in transducing signals from the IR that control glucose homeostasis in insulin-sensitive tissues.^{49,50} However, previous reports have also documented a role for p110 β in transducing signals from the IR controlling cytoskeletal rearrangements.⁵¹ The most likely explanation for these apparent discrepancies are differences in PI3K isoform expression between the tissues/cell systems studied, since expression of p110 α was detected only weakly in a subset of the AML cell lines and blasts studied here, and insulin-sensitive tissues may not express p110 δ . Reports concerning the expression of the PI3K antagonist PTEN in AML blasts are controversial. While variable or nondetectable PTEN expression levels have been reported in individual AML cases,²⁷ a subsequent study found PTEN expression in all AML cases investigated.²⁸ The latter findings are in line with the results obtained in the present study.

Together our data document a novel role for autocrine IGF-I/IGF-IR signaling in the biology of human AML, which may provide novel therapeutic targets to inhibit the proliferation of leukemic cells.

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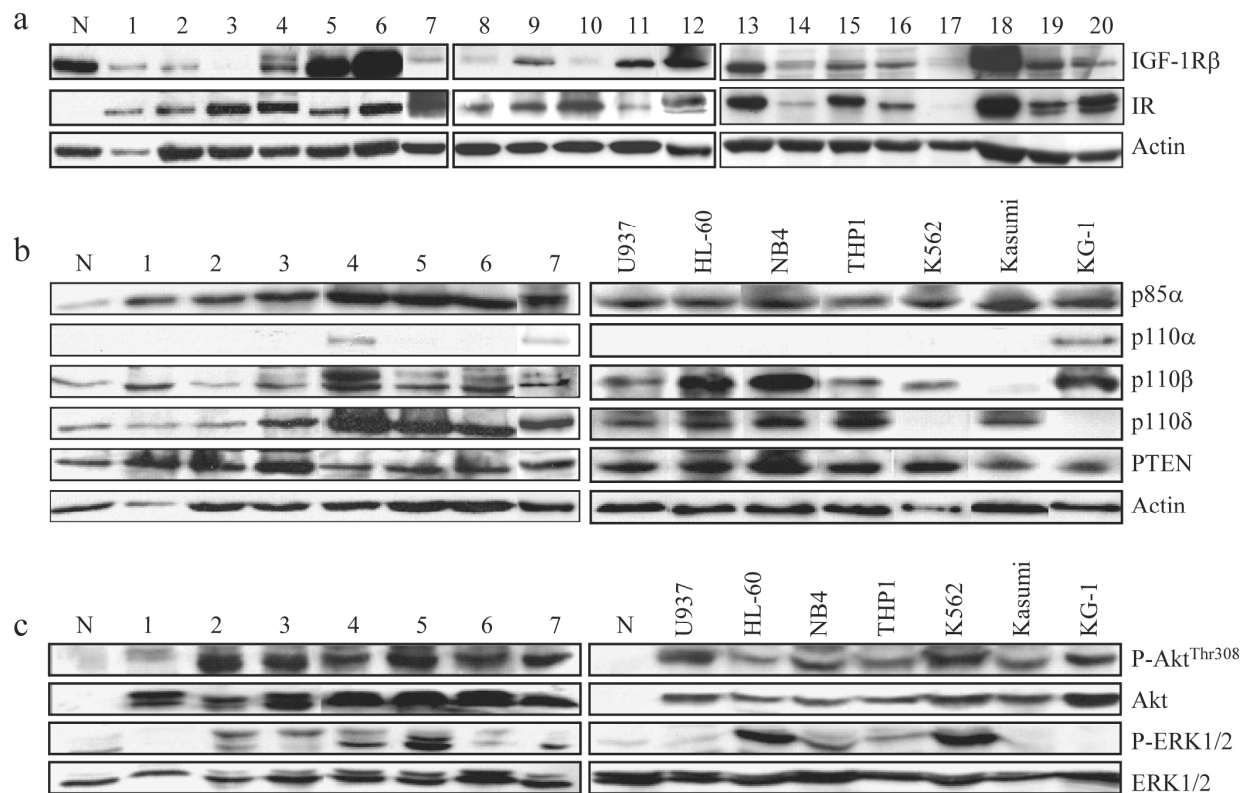
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Supplementary information accompanies the paper on the Leukemia web site (<http://www.nature.com/leu>)

Supplementary Figure 1



Supplementary Figure 1 (a) Expression of IGF-1R β and IR in 20 human AML patient blast cells and normal bone marrow cells (N). (b) PI3K class I α regulatory subunit p85 α , catalytic subunits p110 α , p110 β , p110 δ and the PI3K antagonist phosphatase and tensin homolog (PTEN). (c) Pathway activation monitored by the phosphorylation status of protein kinase B (PKB/Akt: Thr308) and extracellular signal-regulated kinase (Erk: Thr202/Tyr204). Actin was used as a loading control.

Supplementary Table 1

French-American-British (FAB) classification of the AML patient blast cells under study.

Patient	FAB
1	M0
2	M0
3	M0
4	M4
5	M1
6	M4
7	M1
8	M2
9	M4
10	M5
11	M2
12	M5
13	M5
14	M1
15	M1
16	M4
17	M2
18	M5
19	M2
20	M2

3.3. Targeting PI3KC2 impairs proliferation and survival in acute leukemia, brain tumours and neuroendocrine tumours

(British Journal of Cancer; Manuscript submitted)

Targeting PI3KC2 β impairs proliferation and survival in acute leukemia, brain tumours and neuroendocrine tumours

Running Title: PI3KC2 β in human cancers

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ABSTRACT

Eight mammalian phosphoinositide 3-kinase (PI3K) isoforms exist which are subdivided into three classes. While much attention has been given to the class I isoforms, little is known about the functions of class II PI3Ks in human cancer. The expression pattern and functions of the PI3KC2 β isoform were investigated in a panel of tumour samples and cell lines. Over-expression of PI3KC2 β was found in subsets of tumours and cell lines from acute myeloid leukemia (AML), glioblastoma multiforme (GBM), medulloblastoma (MB), neuroblastoma (NB), and small cell lung cancer (SCLC). Specific pharmacological inhibitors of PI3KC2 β or small interfering RNA (siRNA) impaired proliferation of a panel of cell lines and primary cultures from AML, brain tumours and neuroendocrine tumours. Inhibition of PI3KC2 β also induced apoptosis in AML and GBM cell lines and sensitised the cells to chemotherapeutic agents. Furthermore, PI3KC2 β inhibition impaired the phosphorylation of downstream signalling mediators in AML. Together, these data show that PI3KC2 β contributes to proliferation and survival in AML, brain tumours and neuroendocrine tumours and may represent a novel target in these malignancies.

Keywords: PI3KC2 β , pharmacological inhibition, cell proliferation, migration

INTRODUCTION

Phosphoinositide 3-kinases (PI3Ks) play an essential role in the signal transduction events initiated by the binding of extracellular signals to their cell surface receptors (Katso et al., 2001; Vanhaesebroeck et al., 2001). The cellular responses controlled by PI3Ks are extremely diverse, including mitogenesis and proliferation, protection from apoptosis and cell motility (Katso et al., 2001; Vanhaesebroeck et al., 2001). There are eight known PI3Ks in humans, which have been subdivided into three classes, based on structural homology and *in vitro* substrate specificity (Vanhaesebroeck et al., 1997a; Vanhaesebroeck & Waterfield, 1999). Class I_A comprises three highly homologous isoforms, p110 α (Hiles et al., 1992), p110 β (Hu et al., 1993) and p110 δ (Chantry et al., 1997; Vanhaesebroeck et al., 1997b), which exist as a heterodimeric complex with a regulatory subunit containing two Src homology-2 (SH2) domains, mediating enzyme association with phosphotyrosine residues in the cytoplasmic domains of activated polypeptide growth factor receptors (Inukai et al., 1996; Otsu et al., 1991; Pons et al., 1995). All class I PI3Ks function as PtdIns(4,5)P₂ 3-kinase *in vivo*, upon activation by receptor tyrosine kinases or serpentine receptors (Hawkins et al., 1992; Stephens et al., 1991). PtdIns(3,4,5)P₃ serves as a docking site for the serine/threonine protein kinase phosphoinositide-dependent protein kinase-1 (PDK-1) which is activated upon binding (Alessi et al., 1997). Several protein kinases have been identified as downstream targets of PDK-1, such as the serine/threonine protein kinase B (PKB) /Akt, which is a key regulator of cell survival, ribosomal protein S6 kinase (S6K), which stimulates protein synthesis and cell growth, glycogen synthase kinase-3 (GSK-3), a key regulator of glycogen synthesis, and a subset of protein kinase C (PKC) isoforms (Le Good et al., 1998; Vanhaesebroeck & Alessi, 2000).

Class II PI3Ks comprise the *Drosophila* PI3K_{68D/Cpk} (MacDougall et al., 1995; Molz et al., 1996), mouse Cpk-m (Molz et al., 1996), and human PI3KC2 α (Domin et al., 1997), PI3KC2 β (Arcaro et al., 1998) and PI3KC2 γ (Misawa et al., 1998; Ono et al., 1998). The hallmarks of class II family members are a substrate specificity restricted to PtdIns and PtdIns(4)P *in vitro*, and a conserved C-terminal C2 domain, involved in phospholipid binding. Recent studies have started to investigate the regulation and functions of class II PI3Ks *in vivo*. Indeed, several reports have shown that class II PI3Ks are downstream targets of activated receptor tyrosine kinases (RTKs), such as the epidermal growth factor receptor (EGFR), platelet-derived growth factor receptor (PDGFR), c-Kit and insulin receptor (IR) (Arcaro et al., 2002; Arcaro et al., 2000; Brown et al., 1999; Katso et al., 2006). Studies in *Drosophila melanogaster* have also

revealed a role for the class II PI3K_{68D} in cell differentiation downstream of the EGFR (MacDougall et al., 2004). Furthermore, recent reports have documented a role for PI3KC2 β in cell migration in mammalian cells via activation of Rho family GTPases and in human cancer cells (Domin et al., 2005; Katso et al., 2006; Maffucci et al., 2005). Studies by others have described a role for PI3KC2 α in Rho activation and contraction in vascular smooth muscle cells (Wang et al., 2006). Analysis of a conditional knock-out mouse of *PIK3C2B*, however, revealed no obvious phenotype despite a fairly ubiquitous deletion of *PIK3C2B* (Harada et al., 2005).

The importance of PI3K signalling in cancer is highlighted by the fact that mutations in the tumour suppressor gene phosphatase and tensin homologue (*PTEN*) occur frequently in human tumors. PTEN is a phosphatase that antagonises the action of PI3K by dephosphorylating the D-3 position of polyphosphoinositides (Cantley & Neel, 1999; Sansal & Sellers, 2004). Moreover, recent reports have described activating mutations in the *PIK3CA* gene encoding the catalytic p110 α isoform of PI3K in a variety of human cancers including breast, colon and ovarian cancers (Broderick et al., 2004; Samuels et al., 2004; Weir et al., 2004).

In the present report we have evaluated the expression of the class II PI3KC2 β isoform in a panel of primary human tumours and cell lines. Furthermore, we have used isoform-specific pharmacological inhibitors and RNAi to inhibit this enzyme in human cancer cell lines. We show for the first time that PI3KC2 β is over-expressed in acute myeloid leukemia, brain tumours and neuroendocrine tumours and that inhibiting this class II PI3K decreases proliferation and survival in cell lines from these cancers.

MATERIALS AND METHODS

Reagents and antibodies

Antibodies and reagents were purchased from the following companies: The PI3KC2 β antibody was described in (Arcaro et al., 1998). Caspase-3, PARP (Santa Cruz Biotechnology, Santa Cruz, CA, USA); activated Akt/PKB (Ser473), activated JNK (Thr183/Tyr185), activated S6 protein (Ser235/236) (Cell Signalling Technology, Danvers, MA, USA); β -actin, β -tubulin (Sigma-Aldrich, St Louis, MO, USA); siGENOME™ siRNA (Dharmacon, Lafayette, CO, USA);. (PIramed, Berkshire, UK); Etoposide (Calbiochem, La Jolla, CA, USA); Doxorubicin (Pfizer AG, Zurich, CH). PI701 (YM185453) and PI702 (YM182832) were provided by Piramed Pharma Limited and their synthetic details will be the subject of a separate publication.

Apoptosis

For detection of apoptosis, cells were incubated for 16-24 hrs in the presence or absence of inhibitors. The cells were lysed and caspase-3 activity was measured using the CaspACE Assay System (Promega). Additionally, samples were analysed by SDS-PAGE and Western blot with anti-caspase-3 or anti-poly(ADP-ribose) polymerase (PARP) antibodies.

Cell culture

Acute myeloid leukemia, neuroblastoma, glioblastoma, medulloblastoma, small cell lung cancer and mammary epithelial cell lines were grown in RPMI or DMEM (Life Technologies/InvitrogenCarlsbad, CA, USA) with 10% (v/v) fetal calf serum (FCS) and penicillin/streptomycin/L-glutamine, and passaged every 3-5 days. DAOY, D341, D425 and D458 medulloblastoma cell lines were grown in MEM Zinc option (Richter's modification) medium supplemented with 10% FCS. For growth factor stimulations cells were incubated overnight in their growth medium with low serum (0.5-1% v/v) or Optimem medium (Life Technologies/Invitrogen) and washed with serum-free medium prior to incubation with growth factors. Heparinized peripheral blood or bone marrow samples were obtained from adult patients with AML. Blast cells were isolated as described previously (Doepfner et al., 2007). Type II human lung pneumocytes (Pardo et al., 2001) were maintained in DCCM-1 medium supplemented with 10% new born calf serum.

Cell proliferation

Cell lines (5×10^3 cells/well) were seeded in 96-well plates and grown for 72h in serum (10%)-containing medium in the presence or absence of inhibitors. The number of viable cells was analysed by means of an MTS assay using the CellTiter 96® Aqueous One Solution Cell Proliferation Assay (Promega, Madison, WI, USA) according to the manufacturer's instructions. Data are mean with SD from 8 repetitions.

Dissociation of brain tumours

Human brain tumours were removed from 4 patients who underwent surgery for tumour resection at the University Hospital Zurich. The procedures were conducted in accordance with the Declaration of Helsinki and approved by the ethics committee of the Canton Zurich. Following removal, tumour tissue was immediately placed in a petri dish, minced mechanically and digested enzymatically with collagenase D and DNase I (Roche Applied Science, Rotkreuz, Switzerland) for 1 hour at 37°C while being stirred with a magnetic bar. The dissociated cells were then sequentially filtered through 100 and 70µm cell strainers (BD Falcon, BD Biosciences, Basel, Switzerland) to remove any tissue debris. Erythrocytes were removed by resuspending and incubating the cells in ice-cold ACK buffer (17 mM Tris-HCl [pH 7.2] containing 144 mM NH₄Cl) for 10 minutes on ice. The cells were washed in PBS and plated in DMEM (Life Technologies/Invitrogen) supplemented with 10% (v/v) heat inactivated fetal calf serum (FCS) and gentamycin (20mg/ml) and passaged every 3-5 days by trypsinization.

DNA Microarray

Total RNA was extracted from 60 medulloblastoma samples (MB) and 3 cell lines (D283, D341, and DAOY) using the Trizol reagent (Invitrogen). After DNase treatment and RNA purification (RNeasy Micro kit, Qiagen), gene expression profiles were obtained on the Affymetrix HG-U133 Plus 2.0 array that contains more than 54000 probe sets for transcripts and variants. Expression data for 9 normal cerebellums analyzed on the same Affymetrix array version were obtained from Gene Expression Omnibus (GEO) database (<http://www.ncbi.nlm.nih.gov/geo/>). Gene expression data for the samples were normalized using the GCRMA procedure. PI3KC2β expression levels for the samples are presented (unlogged data).

Isolation of RNA from tumour samples and RT-PCR

For primary neuroblastoma samples ethical approval to use residual tissue was obtained. RNA later-preserved tumour tissue was available in the Swiss Pediatric Oncology Group tumour bank. All diagnoses were confirmed by histological assessment of the tumour specimen obtained at surgery. Neuroblastoma tissue was disrupted with a sterile disposable tissue grinder (Sage Products, Cary, IL, USA) and homogenised in guanidinium isothiocyanate-containing buffer. Total RNA of cell lines or tumour tissue was isolated using the RNeasy kit (Qiagen, Santa Cruz, CA, USA) according to the manufacturer's protocol. Total RNA (3 µg) from each tumour sample was converted into cDNA using the SuperScript™ First-Strand Synthesis System for PCR according to manufacturer's instructions (Invitrogen, Carlsbad, CA, USA). mRNA expression of PI3KC2β and 18S (internal control gene) was measured in tumour samples and cell lines by TaqMan® Assay-on-Demand™ Gene Expression products (Applied Biosystems, Foster City, CA, USA). The following primers were used (gene - assay ID): PI3KC2beta - Hm00153248_m1; eukaryotic 18S rRNA - Hs99999901_s1. Three replicates were run for each sample in a 96-well format plate. Gene expression assays consisted of a FAM™ dye-labelled TaqMan® MGB probe and two PCR primers. The thermal cycling conditions consisted of an initial denaturation step at 95°C for 10 min and a 50-cycle countdown at 95°C for 15 s and 60°C for 1 min. Each sample was normalised on the basis of its 18S rRNA content. Relative mRNA expression levels were calculated using the comparative threshold cycle (CT) method (Giulietti et al 2001).

PI3K Assays

Recombinant human PI3KC2β was expressed as a glutathione *S*-transferase (GST)-fusion protein in SF9 insect cells and purified as described previously (Arcaro et al., 1998). Recombinant class I PI3K isoforms were expressed and purified likewise. PI3K activity of the different PI3K isoforms was assayed essentially as described (Hayakawa et al., 2007).

SDS-PAGE and Western blot analysis

Cellular lysates were prepared as previously described (Guerreiro et al., 2006) separated by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE), transferred to a hydrophobic polyvinylidene difluoride (PVDF) membrane (Hybond-P; Amersham Biosciences), and immunoblotted with various antibodies according to the manufacturer's protocol. Chemiluminescence was used for visualization using the enhanced

chemiluminescence (ECL) Western blotting detection reagents (Amersham Biosciences) according to the manufacturer's protocol.

Transient expression in AML cells

AML cells were transfected with small interfering RNA (siRNA) targeting PI3KC2 β using the Amaxa Nucleofector system (Amaxa biosystems, Gaithersburg, MD, USA) according to the manufacturer's protocol. Cell Line Nucleofector Kit V was used and program V-001 applied. After 48h cells were lysed in cell lysis buffer in order to visualize protein expression by SDS-PAGE and Western blotting. Besides, cells were analysed for cell proliferation and apoptosis by MTS assay and Caspase-3 measurement 72h after transfection.

Wound healing assay

EpH4 murine epithelial cells stably transfected with the Ha-*Ras* oncogene and induced by TGF- β 1 to undergo epitheliomesenchymal transition (EMT) *in vivo* to establish FibRas cells were previously described in (Maschler et al., 2005). For wound healing assays, cells were plated in 12-well culture plates in complete medium and grown to confluency. A wound was created by scraping cells with a 200 μ l tip. The migration rate was monitored for eight hours by phase contrast microscopy (Leica DM IRBE Inverse, Widefield) either in the presence or absence of inhibitors.

RESULTS

Expression of PI3KC2 β in tumour samples and cell lines

Previous reports had documented increased expression of PI3KC2 β in leukemia, glioblastoma and lung cancer cell lines and tumours (Arcaro et al., 2002; Knobbe & Reifemberger, 2003; Qian et al., 2002). Therefore, the expression of PI3KC2 β was investigated in a panel of tumours and cell lines from AML, neuroendocrine tumours (SCLC and NB) and brain tumours (MB and GBM). In AML, PI3KC2 β was highly expressed in a subset of AML blasts and cell lines (Figure 1A, left panel). Interestingly, PI3KC2 β expression was much lower in non-leukemic bone marrow cells and immortalised B cells (Figure 1A) indicating that AML blasts and cell lines over-express the enzyme. We also reanalysed cDNA microarray data from a previously published study in AML (Valk et al., 2004). PI3KC2 β mRNA expression was found to be higher in certain groups of AML, depending on molecular and cytogenetic abnormalities. AML categories displaying increased expression included FLT3-ITD and EVI1 (77.37; 99.21), as compared to FLT3-TKD (41.51). Increased expression of PI3KC2 β was also found in AML with the cytogenetic abnormalities -7 (99.72), when compared to +8, 11q13, t(8;21), idt(16), or NN (46.86; 39.35; 54.40; 19.80; 60.03). In contrast, there were no significant differences in expression of PI3KC2 β mRNA between AML French-American-British (FAB) classes.

Protein expression analysis of SCLC cell lines revealed elevated PI3KC2 β expression in 2/4 cases when compared to a normal Type II pneumocyte cell line (PN) (Figure 1B, left panel). TaqMan analysis of *PIK3C2B* expression confirmed that mRNA levels are predictive of protein expression (Figure 1B, right panel).

In neuroblastoma (NB) cell lines, Western blot analysis revealed broad expression of PI3KC2 β (Figure 2A). Upon TaqMan analysis *PIK3C2B* was found to be over-expressed at the mRNA level when compared to normal human adrenal gland (5/8 samples with >2-fold expression) (Figure 2B). In primary tumours from children under the age of one year PI3KC2 β showed increased expression (Figure 2C). This distribution was mirrored in data obtained from TaqMan analysis, where increased mRNA expression was found in the same patient subgroup (3/19 samples with >2-fold expression) (Figure 2D).

In glioblastoma multiforme (GBM) cell lines and *ex vivo* cultures PI3KC2 β was found to be over-expressed in a subset of samples when compared to normal human brain or cerebellum (Figure 2E).

In medulloblastoma (MB) cell lines, heterogeneous PI3KC2 β expression was observed (Figure 2F). Microarray analysis of a panel of primary medulloblastoma samples also showed that PI3KC2 β was over-expressed in 16/60 samples compared to normal human cerebellum (Supplemental Figure 1).

Together, these data revealed subgroups of tumours and cell lines displaying PI3KC2 β over-expression, in which the class II PI3K may play a role in regulating proliferation, survival or migration.

Inhibition of cell proliferation by pharmacological PI3KC2 β inhibitors or siRNA targeting PI3KC2 β

To gain insight into the contribution of the class II PI3K isoform PI3KC2 β in cell proliferation, two different isoform-specific pharmacological inhibitors (PI701 and PI702) were used. The specificity of these inhibitors was verified by *in vitro* PI3K assays using purified recombinant preparation of various PI3K isoforms. The IC₅₀ values for specific inhibition of the enzymatic activity of PI3KC2 β were 182 nM for PI701 and 652 nM for PI702 while values above 10 μ M were observed for the other PI3K isoforms (Table I). Both inhibitors also failed to inhibit the activity of mTOR and DNA-PK, with IC₅₀ values above 100 μ M (data not shown). A screen against a panel of 72 protein kinases *in vitro* confirmed that the two compounds are selective for PI3KC2 β . Indeed, they only showed some inhibitory activity, at a concentration of 10 μ M *in vitro*, against anaplastic lymphoma kinase (ALK), c-Raf, p38-regulated/activated kinase (PRAK) and tyrosine protein kinase receptor B (TrkB)* (*PI702 only) (data not shown).

The anti-proliferative activity of both inhibitors was investigated in a panel of 28 cell lines and primary cultures from AML, GBM, MB, NB and SCLC. As controls, non-leukemic bone marrow cells (N), two immortalised B cells lines (FIN COS, 41b MI) and an immortalised Type II pneumocyte cell line (PN) were included. Both inhibitors of PI3KC2 β inhibited cell proliferation in a dose-dependent manner with IC₅₀ values below 10 μ M (PI701: 16/30 cases; PI702: 9/25 cases) (Figure 3 and Table II). The lowest IC₅₀ values were observed in SCLC cell lines, AML blasts and D341 MB cells (Table II). In contrast, the IC₅₀ values observed in control cells (FIN COS, 41b MI, N, PN) were above 10 μ M. In several cases, cell lines with high PI3KC2 β expression were more sensitive to PI701 and PI702, as was the case for AML (U937, NB4), MB (D341), GBM (T98G) and SCLC (H-209, H-510) (Figure 1 and 2, Table II).

Investigation of the effect of PI701 on activation of downstream signalling mediators in AML cell lines showed a dose-dependent decrease in the phosphorylation of key signalling molecules (Figure 4). These include Akt, c-Jun N-terminal kinases (JNK) and ribosomal S6 protein.

Together, these data show that inhibition of PI3KC2 β with selective pharmacological inhibitors impairs proliferation in a subset of human cancer cells with IC₅₀ values compatible with inhibition of the enzyme. This is in line with the finding that the phosphorylation of key signalling molecules is decreased upon treatment with PI701 in AML.

To validate the results obtained with pharmacological inhibitors, small interfering RNA (siRNA) targeting PI3KC2 β was tested in a AML cell line. The specific down-regulation of PI3KC2 β expression by siRNA was verified by Western blot analysis (Figure 5A). Decreased expression of PI3KC2 β in U937 resulted in a 40% reduction of cell proliferation and was accompanied by increased caspase-3 activity (Figure 5B). The effects of the PI3KC2 β siRNA on cell proliferation were less marked in THP1 cells, which displayed lower expression of the enzyme (data not shown).

Targeting PI3KC2 β enhances the sensitivity of AML and GBM cells to chemotherapy

We next investigated whether inhibition of PI3KC2 β by pharmacological inhibitors could modulate the sensitivity of AML and GBM cells to chemotherapeutic agents. In AML cell lines, combination treatment with PI701 led to markedly increased sensitivity to etoposide (Figure 6A). This effect was also observed in GBM cell lines and *ex vivo* cultures where PI701 combined with doxorubicin had a stronger effect on cell viability than the chemotherapeutic agent alone (Figure 6B and 6C). Moreover, the combination treatment enhanced the induction of apoptosis as assessed by increased caspase-3 activation and poly (ADP-ribose) polymerase (PARP) cleavage (Figure 6D and 6E).

In summary, these results highlight the importance of PI3KC2 β in regulating the viability and chemoresistance of various tumour cells.

PI3KC2 β contributes to cell migration in transformed epithelial cells

Previous reports have described a role for PI3KC2 β in the migration of cancer cells (Katso et al., 2006; Maffucci et al., 2005). To investigate the specific contribution of PI3KC2 β in the migration of tumourigenic vs. non-tumourigenic cells, murine epithelial cells sequentially transformed by oncogenic H-Ras and TGF- β 1 were used (Maschler et al., 2005). To analyse

the contribution of PI3KC2 β to the migratory capacity of cancer cells, murine epithelial cells were treated with PI701. Western blot analysis revealed increased PI3KC2 β expression in the FibRas cells, which have previously been shown to display enhanced migration and invasion, as compared to Eph4 and EpRas cells (Maschler et al., 2005) (Figure 7A). Treatment with PI701 impaired migration of FibRas cells but had no significant effect on the migration of Eph4 and EpRas cells (Figure 7B). At the concentrations used, PI701 did not significantly inhibit cell proliferation (data not shown). The finding that pharmacological inhibition of PI3KC2 β impaired the migratory capacity of highly invasive cells emphasises the importance of PI3KC2 β in regulating cancer cell migration.

DISCUSSION

To date, the class I_A isoform p110 α is the only validated target of the PI3K family in the context of human cancer. Other class I_A isoforms have been associated with a role in various malignancies, including p110 β in colon cancer, and p110 δ in AML and breast cancer. Concerning the class II PI3Ks, PI3KC2 α has been shown to play a role in survival of HeLa cells and increased expression of PI3KC2 β was reported in a subset of tumours and cell lines from AML, GBM and SCLC (Arcaro et al., 2002; Knobbe & Reifemberger, 2003; Qian et al., 2002). Furthermore, PI3KC2 β has been shown to play a role in the migration of A-431, HeLa and ovarian cancer cells, and to contribute to SCLC cell growth and Akt activation in response to growth factors such as SCF (Arcaro et al., 2002; Katso et al., 2006; Maffucci et al., 2005). In the present study, we have extended these studies on PI3KC2 β in AML, brain tumours and neuroendocrine tumours.

Here we report that PI3KC2 β is overexpressed in a variety of human cancer cell lines and primary cultures compared to control tissue. The growing interest in small molecule inhibitors has led to the development of a plethora of pharmacological PI3K inhibitors whose activity in human cancer remains to be validated. In the present study, the effect of two specific inhibitors of PI3KC2 β (PI701, PI702) on cancer cell responses was investigated. Upon treatment with either compound a dose-dependent inhibition of cell proliferation was observed in various human tumour cells while non-tumourigenic cells such as immortalised B cells or type II pneumocytes remained largely unaffected. Moreover, a correlation between protein expression levels and sensitivity to the inhibitors was observed in a number of cell lines. In AML, siRNA against PI3KC2 β also led to decreased proliferation accompanied by an increase in apoptosis. The finding that the activation status of important signalling molecules including Akt, JNK and S6K was reduced upon treatment with PI701 is in line with the inhibitory effect of this compound on cell proliferation.

Interestingly, cotreatment of cells with PI701 led to an increased sensitivity to chemotherapeutic agents such as etoposide and doxorubicin. This supports previous reports showing that the inhibition of important survival pathways, including PI3K/Akt, can enhance the response to cytotoxic reagents (Abdul-Ghani et al., 2006; Kumar et al., 2005). In the present study we have demonstrated for the first time that PI3KC2 β inhibitors can sensitise human cancer cells to chemotherapeutic agents such as etoposide and doxorubicin.

Besides its role in regulating cell proliferation, in invasive murine breast cancer cell lines PI3KC2 β was also found to be involved in cell migration. Enhanced expression of PI3KC2 β was detected in the most motile cells (FibRas) as compared to non-invasive cells (EpH4). Treatment of these cells with increasing doses of PI701 strongly reduced the migratory capacity in wound healing assays. This is an interesting observation considering that malignant cells often acquire the ability to migrate leading to the propagation of metastases throughout the body.

In summary, the present study illustrates that PI3KC2 β plays a crucial role in regulating various cellular responses in a broad spectrum of human cancer cells. Since the pharmacological inhibitor PI701 not only reduced basal cell proliferation but also had an effect on chemosensitivity and cellular migration, PI3KC2 β could prove to be an attractive target for cancer treatment in the future.

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FIGURE LEGENDS

Figure 1 PI3KC2 β expression in AML and SCLC cells. Western blot analysis of PI3KC2 β expression in (A) normal bone marrow cells (N), primary blasts (1-7), AML cell lines and immortalized B cells (FIN COS, 41b MI) and (B) type II pneumocytes (PN) and SCLC cell lines (left panel). Relative mRNA expression levels of *PIK3C2B* in (A) human AML cell lines and (B) SCLC cell lines (right panel). Nontransformed type II human pneumocytes were used as a control.

Figure 2 PI3KC2 β expression in tumours of the central nervous system. In (A-B) neuroblastoma cell lines and (C-D) primary tumour samples, PI3KC2 β expression was analysed both by Western blot analysis (A, C) as well as quantitative RT-PCR (B, D). PI3KC2 β protein expression in (E) glioblastoma cell lines and *ex vivo* cultures and (F) medulloblastoma cell lines by Western blot analysis. For neuroblastoma samples, human adrenal tissue (AG) was used as a control. For glioblastoma and medulloblastoma samples, normal human cerebellum served as a control.

Figure 3 Titration curve of PI701 in AML and SCLC. (A) AML cell lines (U937, triangles; HL-60, circles) and patient blasts (FAB M1, asterisks) and (B) SCLC cell lines (H209, triangles; H510, circles) were treated with increasing concentration of the inhibitor for 72 hours. For (A) AML cell lines and blast cells, immortalised B cells (diamonds and squares) served as a control. For (B) SCLC, nontransformed type II pneumocytes (squares) were used as a control.

Figure 4 Effect of PI701 on the phosphorylation of downstream signalling molecules. AML cell lines (U937 and THP1) were treated with increasing concentrations of PI701 overnight. Pathway activation was visualised by monitoring the phosphorylation status of Akt (P-AktSer⁴⁷³), JNK (P-JNK^{Thr183/Tyr185}) and S6 protein (P-S6 protein^{Ser235/236}).

Figure 5 Inhibition of AML cell proliferation by small interfering RNA (siRNA) targeting PI3KC2 β . (A) U937 cells transfected with control siRNA or siRNA targeting PI3KC2 β were analyzed by western blotting for protein expression. (B) Cell proliferation of U937 cells

transfected with siRNA targeting PI3KC2 β was analysed by MTS assay (left panel) and caspase-3 activity was assessed in parallel. **P<0.01 by analysis of variance test.

Figure 6 PI701 sensitises AML and glioblastoma cells to chemotherapeutic agents. **(A)** Titration curve of U937 (left panel) or THP1 (right panel) cells incubated with increasing concentrations of etoposide in the absence (black circles) or presence (white circles) of PI701 (1 μ M). **(B)** Titration curve of T98G (left panel) or U251 (right panel) cells incubated with increasing concentrations of doxorubicin in the absence (black circles) or presence (white circles) of PI701 (1 μ M). **(C)** Titration curve of two glioblastoma *ex vivo* cultures incubated with increasing concentrations of doxorubicin in the absence (black circles) or presence (white circles) of PI701 (1 μ M). A representative experiment (out of three) performed with eight repetitions is shown for A-C. *P<0.05 or **P<0.01 by analysis of variance test. **(D)** T98G cells were treated with PI701 or doxorubicin alone or in combination and caspase-3 cleavage was evaluated by means of a Western blot. **(E)** U937 cells were treated with increasing concentration of etoposide either alone or in combination with PI701 and PARP cleavage was visualised by means of a Western blot. The band corresponding to cleaved PARP (85 kDa) is shown.

Figure 7 Role of PI3KC2 β expression in mammary epithelial cell lines. **(A)** Western blot analysis of PI3KC2 β expression in EpH4, EpRas and FibRas cells. **(B)** Effect of PI701 on migration of mammary epithelial cell lines. Cells were treated with increasing concentrations of PI701 and the distance migrated was measured after 8 hours.

Supplemental Figure 1 Microarray analysis of PI3KC2 β expression in a panel of primary medulloblastoma samples and cell lines. Gene expression profiles were obtained by using the Affymetrix HG-U133 Plus 2.0 array.

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Table I IC₅₀ values (μM) against isolated enzymes.

Compound	PI3KC2β	p110α	p110β	p110γ	p110δ
PI701	0.528	> 10	> 10	> 10	> 10
PI702	0.632	> 10	> 10	> 10	> 10

Table II IC₅₀ values (μM) of PI701 and PI702 against a panel of cancer cell lines and primary cultures from NB, GBM, MB, AML, and SCLC.

IC50 Values		
	PI701	PI702
Neuroblastoma Cell Lines		
CHP134	7.4	8.0
LAN1	8.3	10.0
SHSY5Y	15.8	6.6
WAC2	5.2	6.0
Glioblastoma Cell Lines and <i>ex vivo</i> Cultures		
T98G	6.9	> 20
U251	8.0	> 20
LN319	19.6	14
LN229	6.2	14.1
U87	> 20	10.2
LO	11.6	ND
RE	13.2	ND
SB	18.2	ND
Medulloblastoma Cell Lines		
DAOY	10.1	> 20
D341	4.5	4.0
AML Cell Lines, Patient Blasts and Control Cells		
U937	3.2	5.5
HL-60	9.6	12.4
NB4	5.3	7.8
THP1	8.4	9.5
Kasumi	> 20	ND
KG-1	17.0	8.0
K562	10.4	> 20
FIN COS	> 20	> 20
41b MI	> 20	> 20
FAB M5	2.5	ND
FAB M1	3.6	ND
FAB M0	ND	6.2
N	ND	12.6
SCLC Cell Lines and Control Cells		
H69	4.4	ND
H209	4.3	ND
H510	5.0	ND
SW2	10.2	ND
PN	12.0	ND

LO, RE, SB = glioblastoma *ex vivo* cultures; FIN COS, 41b MI = immortalised B cells; FAB = French-American-British classification; N = non-leukemic bone marrow cells; PN = immortalised Type II pneumocytes; ND = not determined

Figure 1

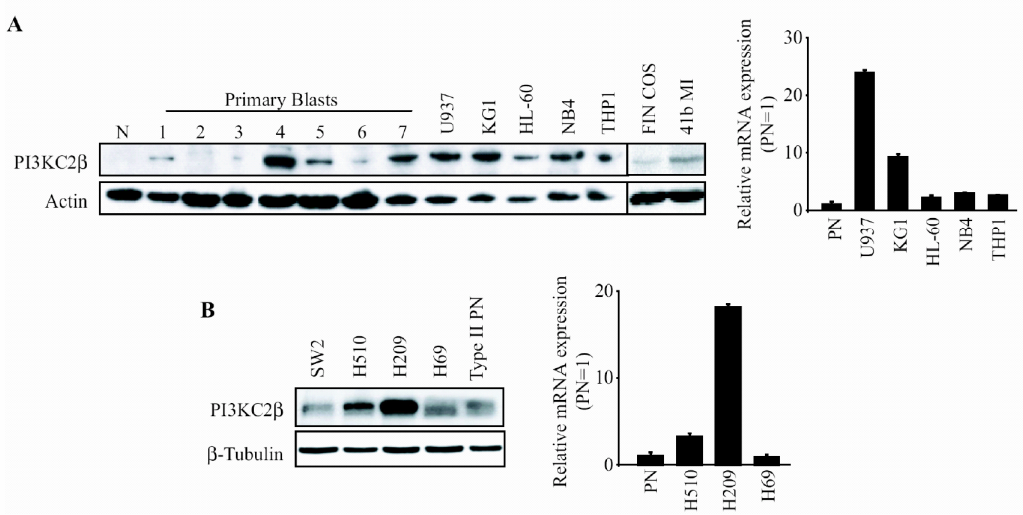


Figure 2

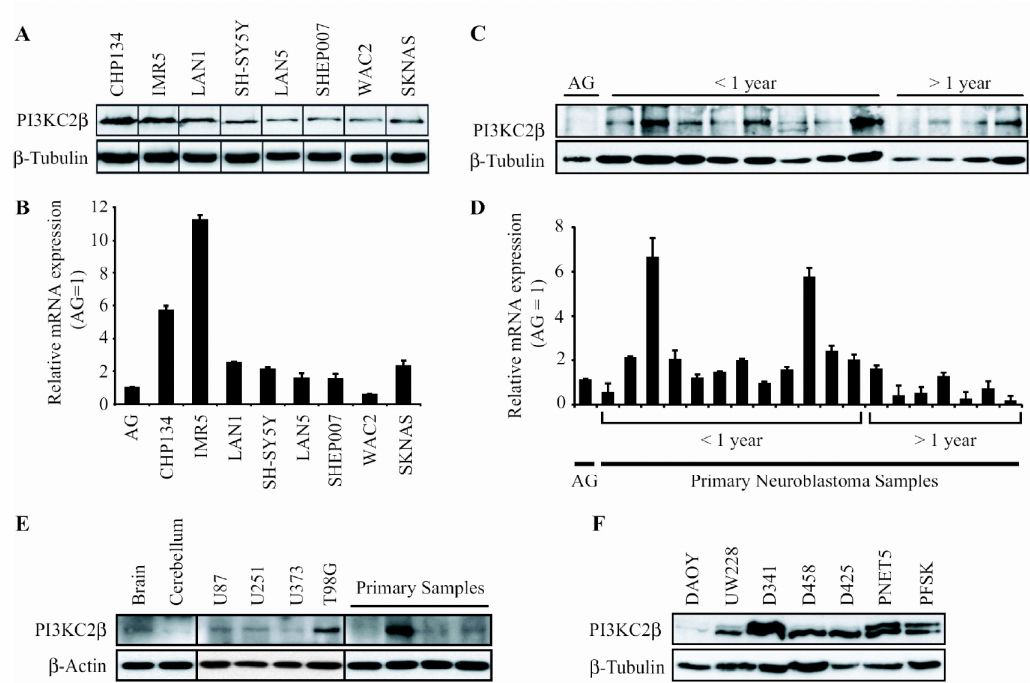


Figure 3

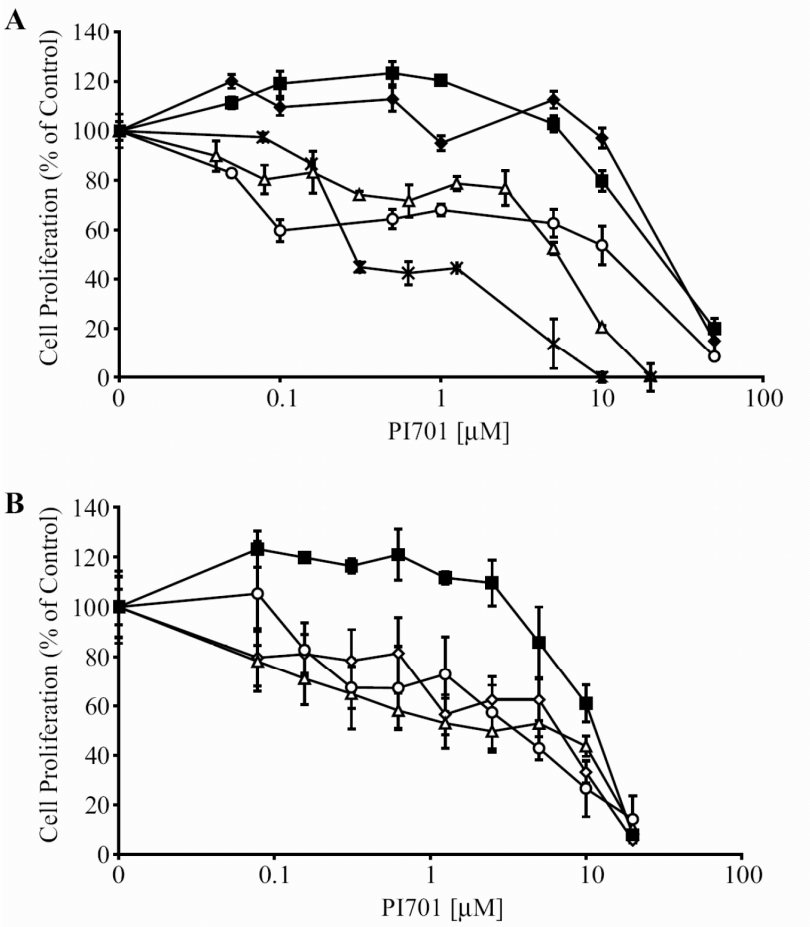


Figure 4

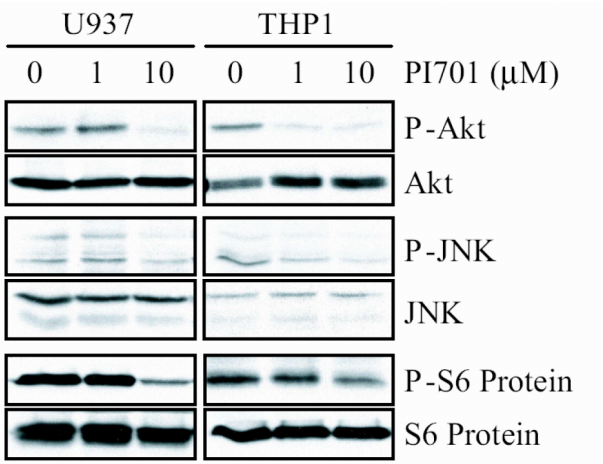


Figure 5

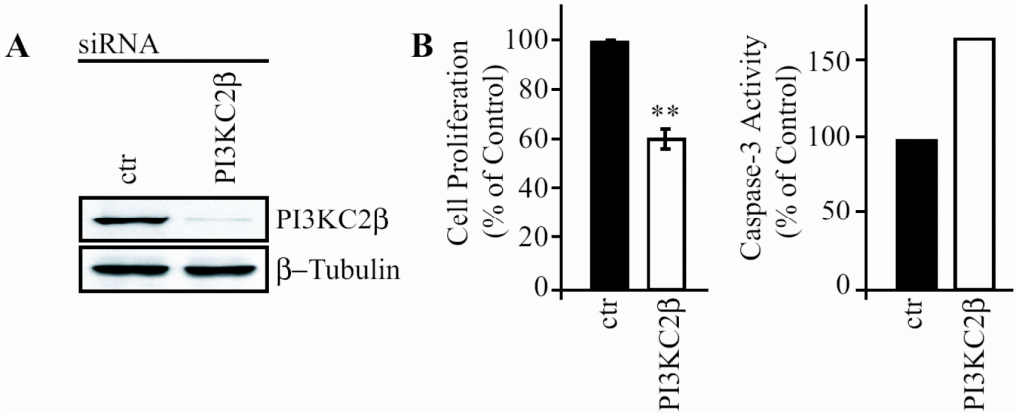


Figure 6

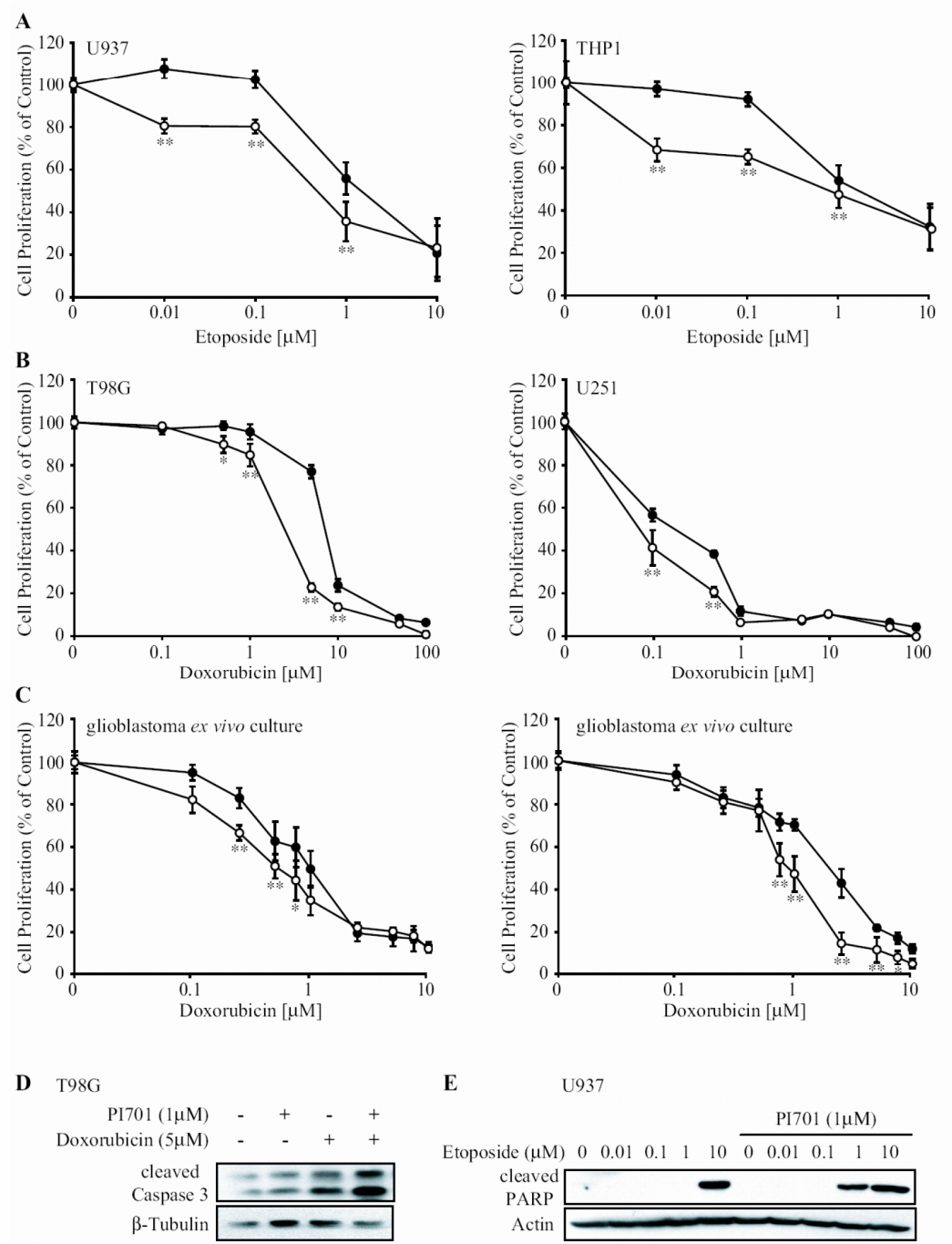
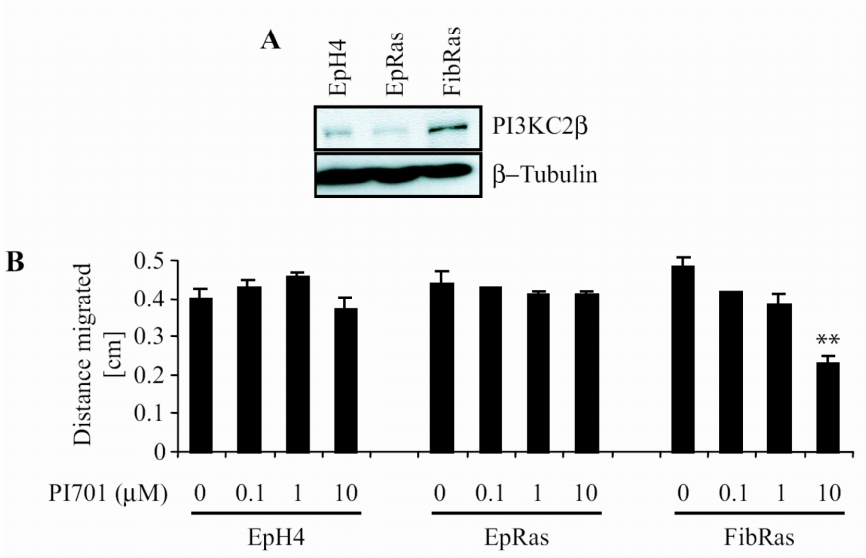
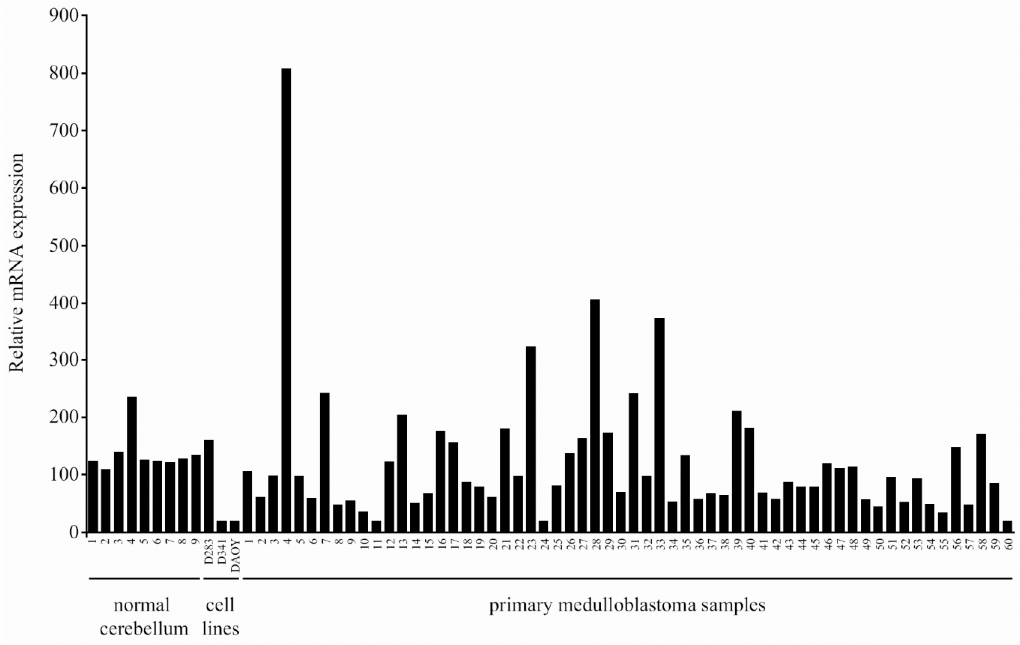


Figure 7



Supplemental Figure 1



3.4. Investigation of the Molecular Determinants of Rapamycin Sensitivity in Acute Myeloid Leukemia Cells
(Manuscript in preparation)

1

Investigation of the Molecular Determinants of Rapamycin Sensitivity in Acute Myeloid Leukemia Cells

Running Title: Rapamycin sensitivity in AML

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ABSTRACT

The mammalian target of rapamycin (mTOR) is a major regulator of cell cycle, proliferation and cell growth. In acute myeloid leukemia (AML) cells, protein expression analysis revealed significant differences in the expression levels of mTOR. Therefore, the role of mTOR in AML cell growth and survival was investigated and cellular responses to the mTOR inhibitor rapamycin were compared in cells expressing high levels of mTOR (mTOR^{high} cells) and cells expressing low levels of mTOR (mTOR^{low} cells). Moreover, an RNAi screen was aimed at uncovering kinases which modulate the sensitivity to rapamycin. Growth factor stimulation revealed impaired phosphorylation of the ribosomal S6 protein and 4E-binding protein (4E-BP) in mTOR^{low} cells. Upon transfection of these cells with a construct encoding mTOR phosphorylation of S6 protein was restored. Nevertheless, rapamycin treatment resulted in a comparable growth reduction and induction of apoptosis in mTOR^{high} and mTOR^{low} cells. Down-regulation of mTOR by siRNA, however, reduced cell growth in mTOR^{high} cells only. Together, these data show an important role of mTOR in a subclass of human AML cells and describe potential molecular targets for cancer therapy in combination with the mTOR inhibitor rapamycin.

INTRODUCTION

The mammalian target of rapamycin (mTOR) is a serine/threonine kinase that controls fundamental cellular processes including transcription, translation, cell size, cell growth, and cytoskeletal organization. TOR was initially isolated by a genetic screen in yeast as a target of the antifungal and immunosuppressant agent rapamycin, a macrocyclic lactone (Heitman et al., 1991). The high specificity of rapamycin for TOR has helped to elucidate the structure and function of this protein and a high conservation of TOR and its signaling network from yeast to mammals could be described. Whereas in *S. cerevisiae* two genes called *TOR1* and *TOR2* could be found (Heitman et al., 1991; Helliwell et al., 1994), one single mammalian homologue, mTOR (also known as RAFT, FRAP and RAPT) was uncovered (Hay & Sonenberg, 2004). Using chemical crosslinking and immunoaffinity purification, mTOR-associated proteins and two different multi-protein complexes, mTORC1 and mTORC2 could be identified in human. The multi-protein complex mTORC1 contains the core components mTOR, mLST8/G β L (G protein β -subunit-like protein) and raptor (Hara et al., 2002; Inoki & Guan, 2006). The activity of mTORC1 is regulated by the integration of signals such as nutrients, growth factors, energy availability and cellular stressors (e.g. hypoxia, osmotic stress, viral infections) (Corradetti & Guan, 2006; Reiling & Sabatini, 2006), and is potently inhibited by rapamycin in complex with the FK506-binding protein FKBP12. Rapamycin together with FKBP12 potently binds to the FRB (FBP12-rapamycin) domain located N-terminal to the kinase domain of TOR leading to the inhibition of its function (Fingar & Blenis, 2004). The mTORC2 complex consists of mTOR, mLST8/G β L and rictor and is believed to be rapamycin-insensitive (Jacinto et al., 2004). Recent findings, however, suppose that prolonged rapamycin exposure (> 24h) can disrupt mTORC2 assembly and function by sequestering newly synthesized mTOR molecules (Sarbasov et al., 2006).

Abnormal activation of signaling pathways both proximal and distal to mTOR frequently occurs in human cancer making this kinase an attractive target for cancer therapies. Different human tumor suppressor proteins such as the tuberous sclerosis complexes (TSC1 and TSC2) or the phosphatase and tensin homologue (PTEN) are known to tightly regulate mTOR. Loss of these tumor suppressors leads to dysregulation of mTOR signaling and results in uncontrolled cell growth and proliferation driving tumorigenesis (Sabatini, 2006; Tee & Blenis, 2005). The acute myeloid leukemia (AML), a cancer of the hematopoietic system, is characterized by an arrest in the differentiation pathway of myeloid progenitors that results in cells that are unable to differentiate into mature functional cells, in particular red blood cells,

leukocytes, and platelets. The development of AML is thought to occur upon two classes of crucial mutational events (Gilliland & Tallman, 2002). Alteration of receptor tyrosine kinase (RTK) signaling (class I mutations) together with mutations in hematopoietic transcription factors (class II mutations) result in increased survival and/or proliferation advantages and are required for the genesis of this leukemia. A constitutive activation of signaling pathways involving mTOR was shown to commonly occur in AML patients (Kubota et al., 2004; Martelli et al., 2006; Min et al., 2003; Zhao et al., 2004). Inhibition of mTOR in AML cells resulted in significant growth inhibition and cell cycle blockage in the G₀/G₁ phase (Recher et al., 2005). Interestingly, the anti-proliferative effect was most pronounced in immature AML cell lines and significant anti-leukemic responses could be induced in poor-risk AML patients upon rapamycin therapy (Recher et al., 2005).

In the present study, the role and function of mTOR and the molecular determinants of rapamycin sensitivity were investigated in AML cells. Expression levels of mTOR were studied in a panel of AML cell lines and the role of this protein on AML cell growth and survival was analyzed. Cells expressing high levels of mTOR were compared to cells expressing low levels of mTOR. Moreover, screening an RNAi kinome library was aimed at identifying human kinases that sensitize AML cells to rapamycin in order to uncover potential new candidates for cancer therapy in combination with the already widely used mTOR inhibitor.

MATERIALS AND METHODS

Reagents and antibodies

Antibodies and reagents were purchased from the following companies: FRAP/mTOR, Akt, ERK, S6 protein, 4E-binding protein, PARP, caspase-3 (Santa Cruz Biotechnology, SantaCruz, CA, USA); activated Akt/PKB (Ser473), activated S6 protein (Ser235/236), activated ERK (42/44), activated 4E-binding protein (Cell Signalling Technology, Danvers, MA, USA); β -actin (Sigma-Aldrich, St Louis, MO, USA); human siARRAY SMARTpool protein kinase library, siGENOME™ siRNA (Dharmacon, Lafayette, CO, USA); NVP-AEW541 (Novartis Pharma AG, Basel, Switzerland); AG1296, piceatannol (Calbiochem, La Jolla, CA, USA); imatinib (BIAFFIN GmbH & Co KG, Kassel, Germany).

Apoptosis

For detection of apoptosis, cells were incubated for 16-24 hrs in the presence or absence of inhibitors. The cells were lysed and caspase-3 activity was measured using the CaspACE Assay System (Promega). Additionally, samples were analysed by SDS-PAGE and Western blot with anti-caspase-3 or anti-poly(ADP-ribose) polymerase (PARP) antibodies.

Cell culture

Acute myeloid leukemia cell lines were grown in RPMI (Life Technologies/InvitrogenCarlsbad, CA, USA) with 10% (v/v) fetal calf serum (FCS) and penicillin/streptomycin/L-glutamine, and passaged every 3-5 days. For growth factor stimulations cells were incubated overnight in their growth medium with low serum (0.5-1% v/v) or Optimem medium (Life Technologies/Invitrogen) and washed with serum-free medium prior to incubation with growth factors. Heparinized peripheral blood or bone marrow samples were obtained from adult patients with AML Blast cells were isolated as described previously (Doepfner et al., 2007b).

Cell proliferation

Cell lines (5 x 10³ cells/well) were seeded in 96-well plates and grown for 72h in serum (10%)-containing medium in the presence or absence of inhibitors. The number of viable cells was analysed by means of an MTS assay using the CellTiter 96® Aqueous One Solution Cell Proliferation Assay (Promega, Madison, WI, USA) according to the manufacturer's instructions. Data are mean with SD from 8 repetitions.

SDS-PAGE and Western blot analysis

Cellular lysates were prepared as previously described (Guerreiro et al., 2006) separated by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE), transferred to a hydrophobic polyvinylidene difluoride (PVDF) membrane (Hybond-P; Amersham Biosciences), and immunoblotted with various antibodies according to the manufacturer's protocol. Chemiluminescence was used for visualization using the enhanced chemiluminescence (ECL) Western blotting detection reagents (Amersham Biosciences) according to the manufacturer's protocol.

siRNA screen

AML cells were transfected with small interfering RNA (siRNA) targeting 779 human kinases (human *siARRAY* SMARTpool protein kinase library) using DharmaFECT transfection reagents (Dharmacon, Lafayette, CO, USA) according to the manufacturer's protocol. 24h post transfection, rapamycin was added and cell proliferation rate was analyzed after 72h by means of a MTS assay.

Transient and stable expression in AML cells

AML cells were transfected with small interfering RNA (siRNA) or small hairpin RNA (shRNA) using the Amaxa Nucleofector system (Amaxa biosystems, Gaithersburg, MD, USA) according to the manufacturer's protocol. After 48h cells were lysed in cell lysis buffer in order to visualize protein expression by SDS-PAGE and Western blotting. Besides, cells were analyzed for cell proliferation and apoptosis by MTS assay and Caspase-3 measurement 72h after transfection. Alternatively, the cells transfected with the shRNA were resuspended in fresh medium containing puromycin at 2 µg/ml and selected for 3–4 weeks to obtain stable transfectants.

RT-PCR analysis

RNA was isolated using the RNeasy Mini Kit (Qiagen, Santa Cruz, CA, USA) from 1×10^6 cells. Reverse transcription–polymerase chain reaction (RT–PCR) was performed according to the QIAGEN OneStep RT–PCR protocol. Expression of mTOR and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was analyzed using the following primers: mTOR-FP, 5'-CTGGGACTCAAATGTGTGCAGTTC-3'; mTOR-RP, 5'-GAACAATAGGGTGAATGATCCGGG-3'; GAPDH-FP, 5'-AACGTGTCAGTGGTGGACCT-3'; GAPDH-RP, 5'-GGGTGTCGCTGTTGAAGTCA-3'.

RESULTS

AML cells express variable levels of the mTOR protein and show differences in signal transduction

Various reports have described a crucial role for the PI3K/Akt/mTOR cascade in human cancer development and aberrant activation of growth-regulating genes upstream and downstream of mTOR have been described in AML (Kubota et al., 2004; Martelli et al., 2006; Min et al., 2003; Zhao et al., 2004). Nevertheless, activating mutations or over-expression of mTOR have not been described so far, nor has mTOR been described to be targeted by recurrent translocations in AML (Recher et al., 2005). Therefore, protein expression of mTOR was investigated in a panel of AML cells and its role in signal transduction was analyzed.

Interestingly, the mTOR protein was found to be expressed with high variability in a panel of seven leukemic cell lines, as assessed by Western blot analysis (Figure 1A, upper panel). In contrast, a RT-PCR analysis revealed that the mRNA levels of mTOR were essentially comparable between the different AML cell lines (Figure 1A, lower panel). Stimulation of AML cells with stem cell factor (SCF) or insulin-like growth factor I (IGF-I) activated the signal transducer Akt, ribosomal S6 protein and the 4E-binding protein (4E-BP) in cells expressing high levels of mTOR (Figure 1B, left panel). In mTOR^{low} cells, however, growth factor stimulation revealed impaired phosphorylation of the mTOR downstream transducers S6 protein and 4E-BP whereas the phosphorylation of the upstream molecule Akt was detectable (Figure 1B, right panel).

Taken together, these results revealed differences in the expression levels and significance of the mTOR protein regarding cell signaling and cellular responses in a subgroup of AML cell lines.

Rapamycin treatment results in a comparable growth reduction in mTOR^{high} and mTOR^{low} cells

Rapamycin and its analogs are well known inhibitors of mTOR and treatment with rapamycin was shown to inhibit cell proliferation in a large number of cell lines, including AML cells (Recher et al., 2005). Therefore, the effect of rapamycin on cell growth and survival was investigated in cells expressing high levels of mTOR and compared to cells expressing low levels of mTOR.

In a panel of AML cell lines treated with increasing concentrations of rapamycin, no significant differences between the two groups of mTOR^{high} and mTOR^{low} cells could be identified. Both groups contained highly sensitive AML cell lines with IC₅₀ between 1-10ng/ml and cell lines that were much less sensitive to rapamycin (IC₅₀ > 100ng/ml) (Figure 2A). In addition to its strong effects on cell proliferation, rapamycin has been shown to induce a cell cycle arrest in G1/G0 and to enhance apoptosis in cancer cells. Analysis of the cell cycle in mTOR^{high} and mTOR^{low} cells did not reveal any striking differences in the amount of dead cells upon treatment with rapamycin. In both groups of AML cell lines, 20ng/ml of the inhibitor lead to an increase in the number of dead cells by around 20% (Figure 2B).

In support of this notion, evaluation of the induction of caspase-3 activity in the two groups of cells after treatment with rapamycin revealed no significant differences suggesting comparable levels of apoptosis induction in mTOR^{high} and mTOR^{low} cells (Figure 2C). However, the G1/G0 cell cycle arrest upon rapamycin treatment was more pronounced in the cells expressing high levels of mTOR compared to the mTOR^{low} cells (Figure 2B).

In summary, rapamycin treatment appears to affect AML cell proliferation and induction of apoptosis independently of the levels of mTOR protein expression.

mTOR is crucial for cell proliferation in mTOR^{high} cells

The striking differences in the expression levels of mTOR in a panel of AML cells lines raised the question of a particular significance of this protein in mTOR^{high} cells. As the use of the mTOR inhibitor rapamycin did not reveal any striking differences between the two groups of cells regarding cellular responses such as cell proliferation or induction of apoptosis, further experiments were aimed at investigating the exact role of the mTOR protein. Therefore, on the one hand, mTOR^{low} cells were transfected with a construct encoding mTOR and on the other hand, mTOR was down-regulated by small interfering RNA (siRNA) targeting mTOR.

Strikingly, upon transfection of mTOR^{low} cells with a construct encoding mTOR (pRK5-mTOR), the phosphorylation of the downstream target S6 protein was restored after 24 hours already (Figure 3A, left panel). Analysis of cell proliferation, however, did not reveal any significant differences in the proliferation rate of the mTOR-transfected cells compared to the cells transfected with a control empty vector (Figure 3A, right panel). Interestingly, the down-regulation of mTOR by siRNA reduced cell proliferation in mTOR^{high} cells but exerted only marginal effects on mTOR^{low} cells (Figure 3B). Whereas the cells expressing only low levels

of mTOR showed no significant difference regarding cell proliferation after down-regulation of the mTOR protein, the cell lines expressing high levels of mTOR significantly reduced their rate of proliferation up to around 50% (Figure 3B).

Together, these results suggest a crucial role of mTOR on cell proliferation in mTOR^{high} cells whereas the subgroup of cells expressing low levels of mTOR is much less dependent on this protein in regard to cell proliferation.

A siRNA screen uncovers kinases which sensitize AML cells to rapamycin

The results obtained above by testing rapamycin in different AML cell lines revealed an overall anti-proliferative and apoptosis inducing effect of this agent, independently of the expression level of the mTOR protein. Therefore, a siRNA screen was aimed at uncovering kinases which modulate the sensitivity of rapamycin and to compare the two groups of cells expressing high or low levels of mTOR.

In a first set-up, two batches of mTOR^{low} HL-60 cells were transfected with a siRNA library targeting 779 human protein and lipid kinases and analyzed for cell proliferation in the absence or presence of rapamycin. The cells transfected with targeted siRNA were compared to cells transfected with a control non-targeting siRNA either in the absence or presence of rapamycin. The data obtained was first used to identify siRNAs which predominantly reduced cell proliferation in combination with rapamycin and thus sensitized the cells to rapamycin. Top candidates could be found in the group of receptor tyrosine kinases such as the insulin like-growth factor receptor I (IGF-IR), fms-like tyrosine kinase 3 (FLT3) and the fibroblast growth factor receptor 1 (FGFR1). Furthermore, signal transducers such as SYK, ZAP70 and AKT1-3 were uncovered as well as the already well known oncogenes in leukemia ABL1 and ABL2 (Figure 4A). Whereas in some cases the down-regulation of the kinase already lead to a decrease in cell proliferation (IGF-IR, FLT3, ABL1), other candidates only reduced the proliferation rate only in combination with rapamycin (Figure 4A). To validate the top candidates, HL-60 cells were transfected with shRNA specifically targeting SYK, ZAP70, FLT3, ABL1, ABL2 or AKT1 and were again analyzed for cell proliferation in the absence or presence of rapamycin. Using this approach, down-regulation of the candidate proteins reduced cell proliferation rate between 10% to around 45%. Nevertheless, the addition of rapamycin further decreased the proliferation (Figure 4B). Interestingly, the analysis of the basal expression of SYK revealed over-expression of the protein in a panel of AML cell lines when compared to control immortalized B cells (Figure 4C).

In summary, screening a protein kinase library uncovered human kinases which sensitize the AML cell line HL-60 to rapamycin. The down-regulation of certain RTKs or RTK signal transducers strengthened the anti-proliferative effect of rapamycin making them interesting candidates for targeted therapies in combination with the mTOR inhibitor.

RTK inhibitors or inhibition of SYK/ZAP70 reduce cell proliferation and sensitize AML cells to rapamycin

In order to investigate the potential of the candidate proteins as molecular targets in combination with rapamycin, HL-60 cells were treated with the pharmacological inhibitors NVP-AEW541, AG1296, imatinib or piceatannol. The effect on signal transduction and cell proliferation rate was investigated in absence or presence of rapamycin. NVP-AEW541 is a specific IGF-IR kinase inhibitor and has already been shown to potently inhibit AML cell growth alone or in combination with chemotherapeutic agents (Doepfner et al., 2007b; Garcia-Echeverria et al., 2004). AG1296 inhibits the activity of the PDGFR, c-Kit, as well as FLT3 (Tse et al., 2002). Imatinib is a well known RTK inhibitor which potently inhibits the BCR-ABL fusion protein in human leukemias as well as the receptors c-Kit and PDGFR (Buchdunger et al., 1996; Fang et al., 2000). Piceatannol has been reported as a SYK/ZAP70-specific kinase inhibitor with anti-tumorigenic potential in different human cancers (Balaian et al., 2003; Wang et al., 1998).

Treatment of HL-60 cells with increasing concentrations of NVP-AEW541, AG1296, imatinib or piceatannol reduced the phosphorylation of the signal transducers Akt and ribosomal S6 protein in a dose-dependent manner (Figure 5A). Therefore, the effect on cellular responses such as the rate of proliferation upon treatment with the inhibitors was tested. HL-60 cells turned out to be highly sensitive to the RTK inhibitor imatinib ($IC_{50} < 1\mu M$), whereas the cells were much less responsive to NVP-AEW541, AG1296 or piceatannol ($IC_{50} \geq 10\mu M$) (Figure 5B). The addition of rapamycin, however, significantly reduced cell proliferation rate in all cases (Figure 5B). Already low concentrations of the inhibitors strongly reduced cell proliferation in combination with rapamycin (10ng/ml).

Taken together, the pharmacological inhibitors NVP-AEW541, AG1296, imatinib and piceatannol affect signal transduction in HL-60 cells, reduce cell proliferation and sensitize the cancer cells to rapamycin.

NVP-AEW541, AG1296, imatinib and piceatannol induce apoptosis in AML cells

In a next step, the role of NVP-AEW541, AG1296, imatinib and piceatannol on the induction of apoptosis was addressed. HL-60 cells were treated with increasing concentrations of the inhibitors and the effect on apoptotic proteins such as PARP and caspase-3 was investigated. Single treatment with NVP-AEW541, imatinib and piceatannol lead to cleavage of PARP and caspase-3 suggesting an induction of apoptosis at concentrations between 1 to 10 μ M (Figure 6A). AG1296, on the other hand, did not show any effect on the cleavage of PARP or caspase-3 when used as a single agent (Figure 6A). Again, also the potential use of the inhibitors in combination with rapamycin was investigated. HL-60 cells treated with rapamycin in addition to NVP-AEW541, AG1296, imatinib or piceatannol displayed highly increased caspase-3 activity after 24 hours (Figure 6B). Interestingly, already at low concentrations of the inhibitors (1 μ M), low concentrations of rapamycin (10ng/ml) significantly increased the activity of caspase-3 as compared to the inhibitor alone (Figure 6B).

Together these data describe the potential of the combinatorial use of the RTK inhibitors NVP-AEW541, AG1296 and imatinib or the SYK/ZAP70 inhibitor piceatannol together with rapamycin as an interesting new anti-proliferative approach in AML.

DISCUSSION

The mammalian target of rapamycin (mTOR) has emerged as an important therapeutic target for cancer (Faivre et al., 2006; Hay, 2005; Rowinsky, 2004). Rapamycin and its derivatives that specifically inhibit mTOR are now being actively evaluated in clinical trials (Faivre et al., 2006; Rowinsky, 2004). However, many cancer cells are resistant to rapamycin and its derivatives. The mechanism of this resistance remains a subject of major therapeutic significance (Easton et al., 2006). It was reported that the inhibition of mTOR by rapamycin triggers the activation of two survival signaling pathways that may contribute to drug resistance. Treatment of human lung cancer cells with rapamycin suppressed the phosphorylation of p70(S6K) and 4E-BP1, indicating an inhibition of mTOR signaling (Sun et al., 2005). Paradoxically, rapamycin also concurrently increased the phosphorylation of both Akt and eIF4E (Sun et al., 2005). The rapamycin-induced phosphorylation of Akt and eIF4E was suppressed by LY294002, suggesting the requirement of PI3K in this process (Sun et al., 2005). The activated Akt and eIF4E appeared to attenuate the growth-inhibitory effects of rapamycin, serving as a negative feedback mechanism. In support of this model, rapamycin combined with LY294002 exhibited enhanced inhibitory effects on the growth and colony formation of cancer cells (Sun et al., 2005). Further work suggested that feedback down-regulation of receptor tyrosine kinase signaling is a frequent event in tumor cells with constitutive mTOR activation (O'Reilly et al., 2006). Reversal of this feedback loop by rapamycin may attenuate its therapeutic effects, whereas combination therapy that ablates mTOR function and prevents Akt activation may have improved antitumor activity (O'Reilly et al., 2006). A recent report showed that rapamycin mediates Akt activation through an IGF-IR-dependent mechanism (Wan et al., 2007). Thus, it was concluded that combinatorial targeting of mTOR and the IGF-IR may be a promising strategy to enhance mTOR-targeted anticancer therapy (Wan et al., 2007).

In the present study, we have systematically investigated the mechanisms underlying the sensitivity or resistance of AML cells to rapamycin. The expression levels of mTOR or the activation status of the mTOR/S6K pathway did not appear to make a major contribution to the sensitivity of AML cell lines to rapamycin. Indeed, AML cells with low mTOR expression levels and low mTOR/S6K pathway activation status were not significantly different from cells with high mTOR expression levels in terms of rapamycin sensitivity. In contrast siRNA-mediated down-regulation of mTOR only significantly affected cell growth in AML cells with high mTOR expression levels.

The use of a siRNA screen to identify modulators of rapamycin sensitivity in AML cells uncovered several potential drug targets for combinatorial approaches. In support of previous reports in other cancer cells, targeting Akt or the IGF-IR by siRNA resulted in a sensitization of AML cells to rapamycin (O'Reilly et al., 2006; Sun et al., 2005; Wan et al., 2007). In addition the siRNA screen uncovered several other RTKs as potential modulators of rapamycin sensitivity of AML cells. These RTKs included the FGFR and FLT3, which have previously been shown to be involved in AML cell responses (Doepfner et al., 2007a). Using pharmacological inhibitors of these RTKs, it was possible to sensitize AML cells to rapamycin, confirming the results obtained with siRNA. Since the ABL kinases were identified in the siRNA screen for modulators of rapamycin sensitivity in AML, the combinatorial use of Gleevec, which inhibits ABL with rapamycin may represent a promising drug combination in AML. The combinatorial use of rapamycin derivatives with RTKs has been reported in other systems, such as in glioblastoma in the case of EGFR inhibitors (Wang et al., 2006). Other non-receptor tyrosine kinases of the SYK/ZAP70 family of kinases were also identified in the screen, which led to the validation of SYK/ZAP70 inhibitors (piceatannol) with rapamycin. It is of interest to note here that SYK has been previously shown to be involved in the activation of the mTOR pathway in lymphoma (Leseux et al., 2006), which was supported by the finding that piceatannol potently impaired activation of the S6K pathway in AML cells.

In summary, the present study described the potential of using RNAi screens to identify novel drug targets for combinatorial use with rapamycin and identified several promising drug combination in AML, which warrant further investigations.

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FIGURE LEGENDS

Figure 1 Acute myeloid leukemia (AML) cell lines show variable expression levels of the mammalian target of rapamycin (mTOR) and differences in the response to growth factors. (A) Seven AML cell lines (U937, HL-60, NB4, THP1, K562, Kasumi, KG-1) were analyzed by western blotting (upper panel) and RT-PCR (lower panel) for mTOR. Actin and GAPDH was used as a loading control. (B) AML cells expressing high or low levels of mTOR (mTOR^{high}, NB4; mTOR^{low}, U937) were stimulated with stem cell factor (SCF) and insulin-like growth factor I (IGF-I). Pathway activation was monitored by the phosphorylation status of Akt, S6Protein and the 4E-binding protein (4E-BP).

Figure 2 Inhibition of AML cell proliferation and induction of apoptosis by the mTOR inhibitor rapamycin. (A) Cell proliferation rate was analyzed by means of an MTS assay in AML cell lines incubated with increasing concentration of rapamycin. (B) AML cells with low or high levels of mTOR (mTOR^{low}, U937, HL-60; mTOR^{high}, THP1) were incubated with increasing concentrations of rapamycin and DNA fragmentation was analyzed by detection of cells with fractional (Sub-G1) DNA content using propidium iodide (PI) staining and FACS analysis. (C) AML cells were incubated with increasing concentrations of NVP-AEW541 and analyzed for caspase-3 activity.

Figure 3 Transfection of AML cells with a construct encoding mTOR or small interfering RNA (siRNA) targeting mTOR. (A) AML cells expressing low levels of mTOR were transfected with a construct encoding mTOR (pRK5-mTOR) and analysed for phosphorylation of the downstream target S6Protein by Western blot (left) or cell proliferation by means of an MTS assay (right). (B) AML cells with low or high levels of mTOR (mTOR^{low}, HL-60, U937; mTOR^{high}, THP1, NB4) were transfected with siRNA targeting mTOR. Cell proliferation rate was analyzed by MTS assay (left) and the downregulation of the protein was validated by Western blot (right). **p<0.01 by analysis of variance test.

Figure 4 A siRNA screen to uncover kinases which sensitize AML cells to rapamycin. (A) HL-60 cells were transfected with a protein kinase library targeting 779 human kinases and cell proliferation rate was analyzed in the absence or presence of rapamycin. Top candidates which reduced cell proliferation in addition to rapamycin are listed in a table. Numbers are

percentage of cells transfected with a non-targeting siRNA in the absence or presence of rapamycin. **(B)** HL-60 cells were transfected with shRNA targeting some of the top candidates from the siRNA screen or a control non-targeting shRNA. Cell proliferation rate was measured in the absence or presence of rapamycin by means of a MTS assay after 72h (upper panel). Downregulation of the protein was validated by Western blot after 48h (lower panel). **(C)** Syk protein expression analyzed by Western blot in a panel of AML cell lines. Immortalized B cells (FIN COS, 41b MI) were used as control cells.

Figure 5 Pharmacological inhibitors targeting candidates of the siRNA screen were used to analyze the effect on pathway activation and proliferation rate in the absence or presence of rapamycin. **(A)** HL-60 cells were treated with increasing concentration of NVP-AEW541, AG1296, imatinib or piceatannol and the phosphorylation of the signal transducer Akt and ribosomal S6 protein was analyzed by Western blot after 24h. **(B)** HL-60 cells were incubated with increasing concentrations of NVP-AEW541, AG1296, imatinib or piceatannol in the absence (black signs) or presence (white signs) of rapamycin and cell proliferation rate was measured by means of a MTS assay after 72h. Alternatively, the number of viable cells was counted after staining with Trypan blue after 72h. * $p < 0.05$ or ** $p < 0.01$ by analysis of variance test.

Figure 6 Pharmacological inhibitors targeting candidates of the siRNA screen were used to analyze the effect on apoptosis. **(A)** HL-60 cells were treated with increasing concentration of NVP-AEW541, AG1296, imatinib or piceatannol and the cleavage of PARP or caspase-3 was analyzed by Western blot after 24h. **(B)** HL-60 cells were incubated with increasing concentrations of NVP-AEW541, AG1296, imatinib or piceatannol in the absence or presence of rapamycin and analyzed for caspase-3 activity after 24h. * $p < 0.05$ or ** $p < 0.01$ by analysis of variance test.

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Figure 1

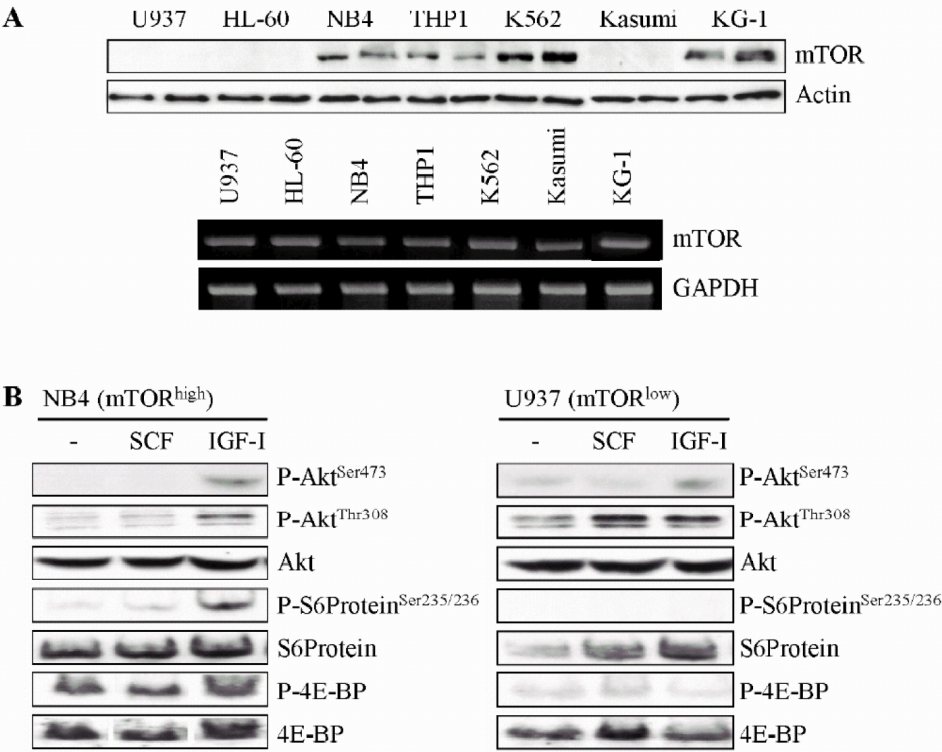


Figure 2

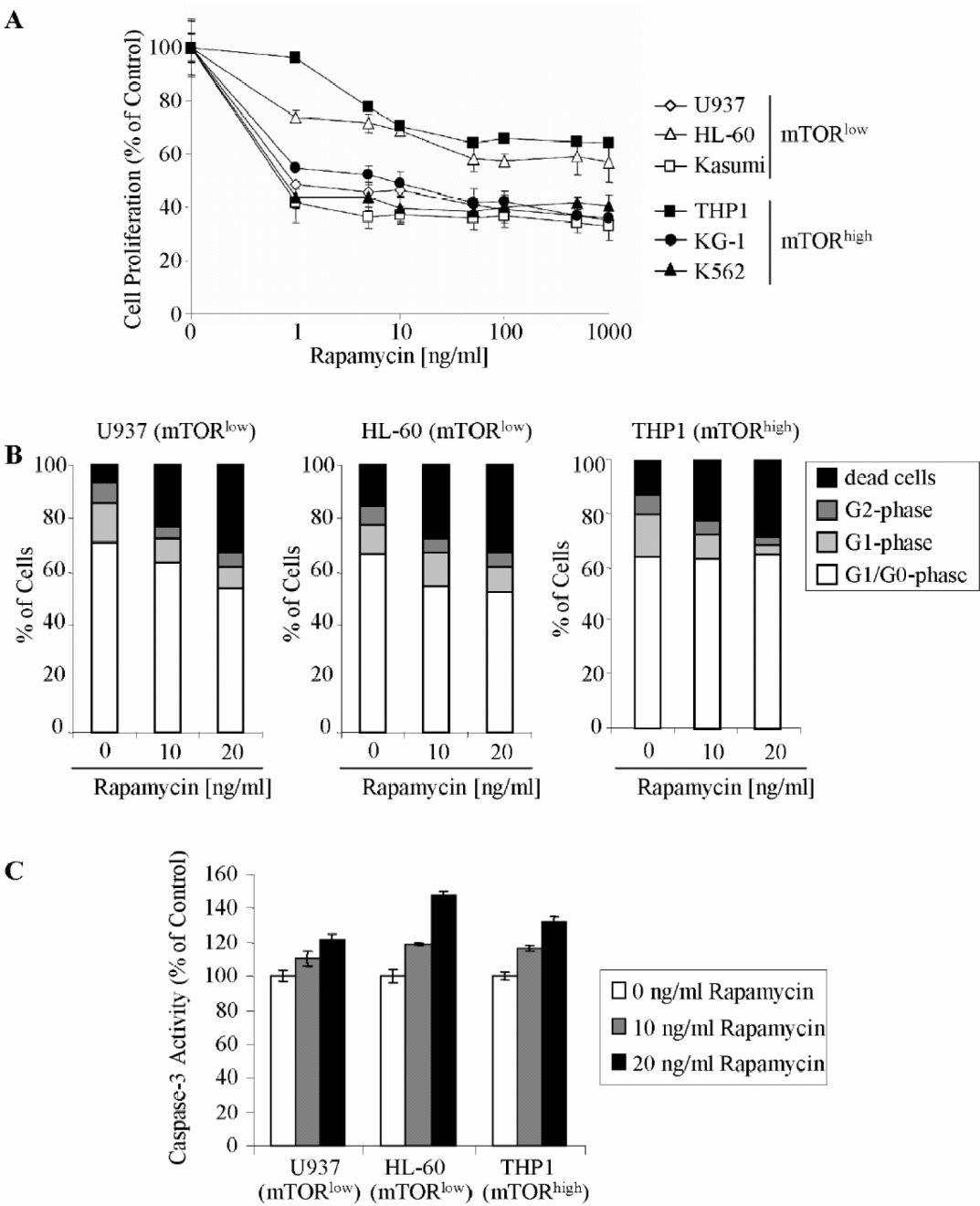


Figure 3

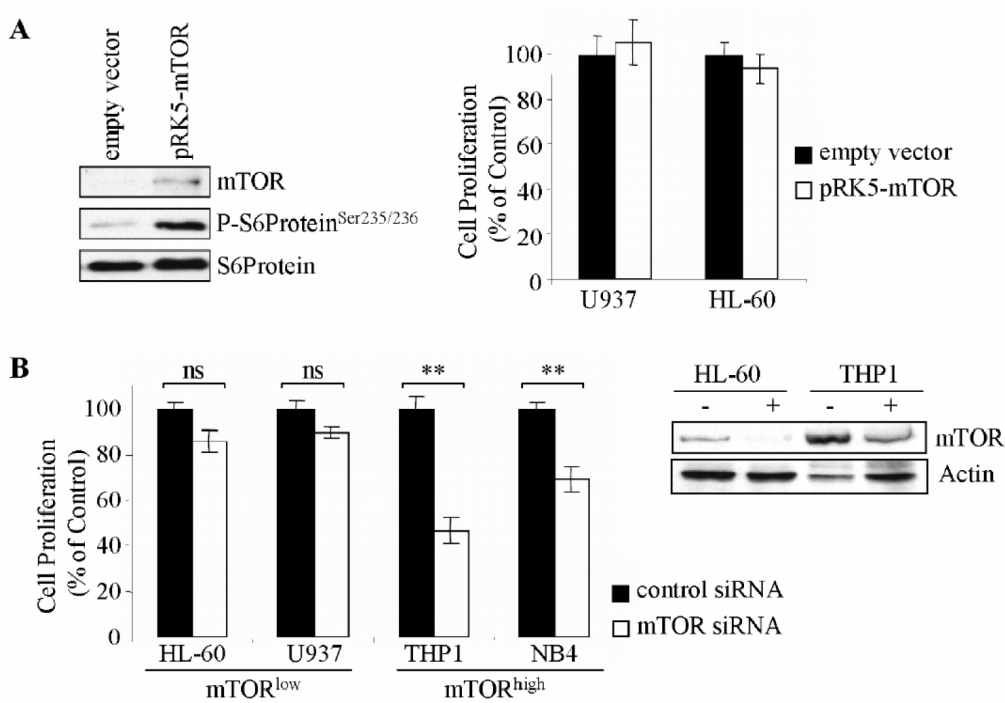


Figure 4

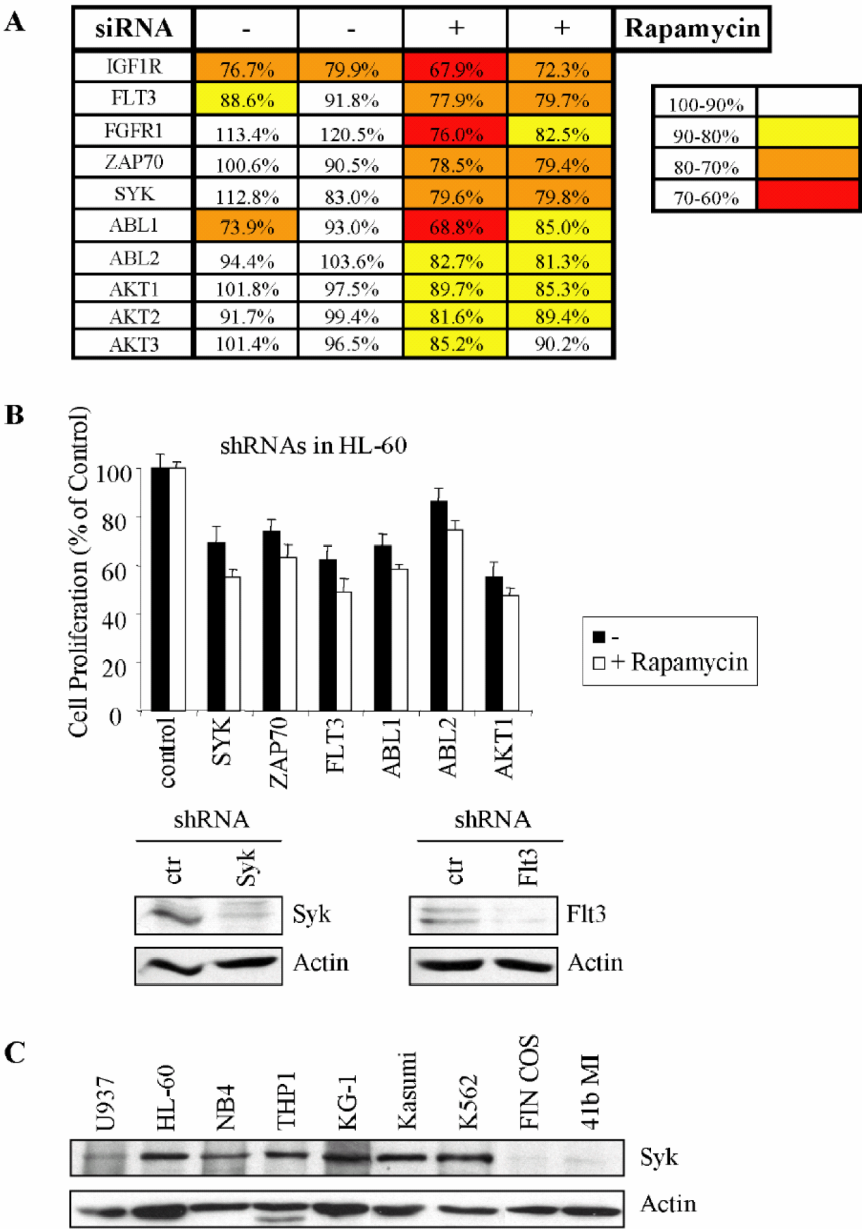


Figure 5

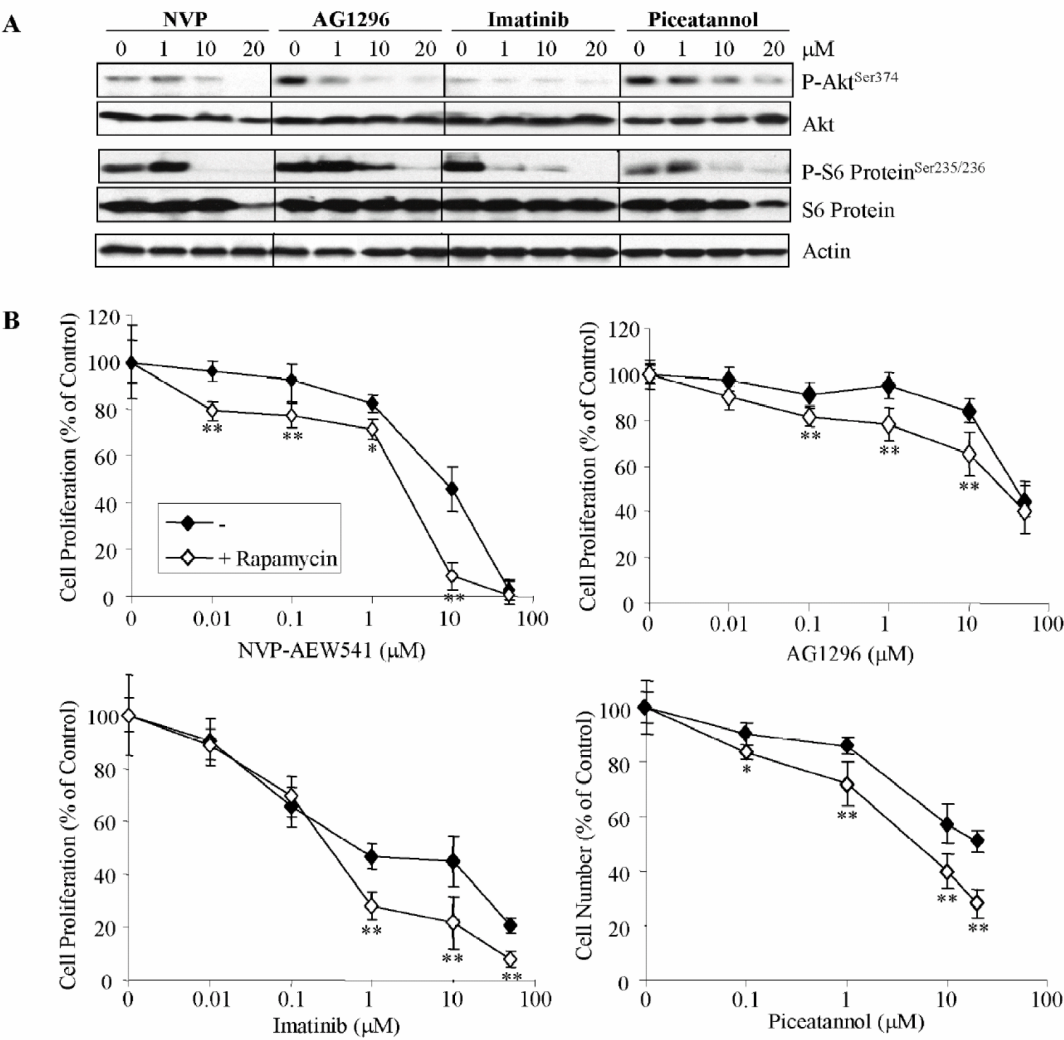
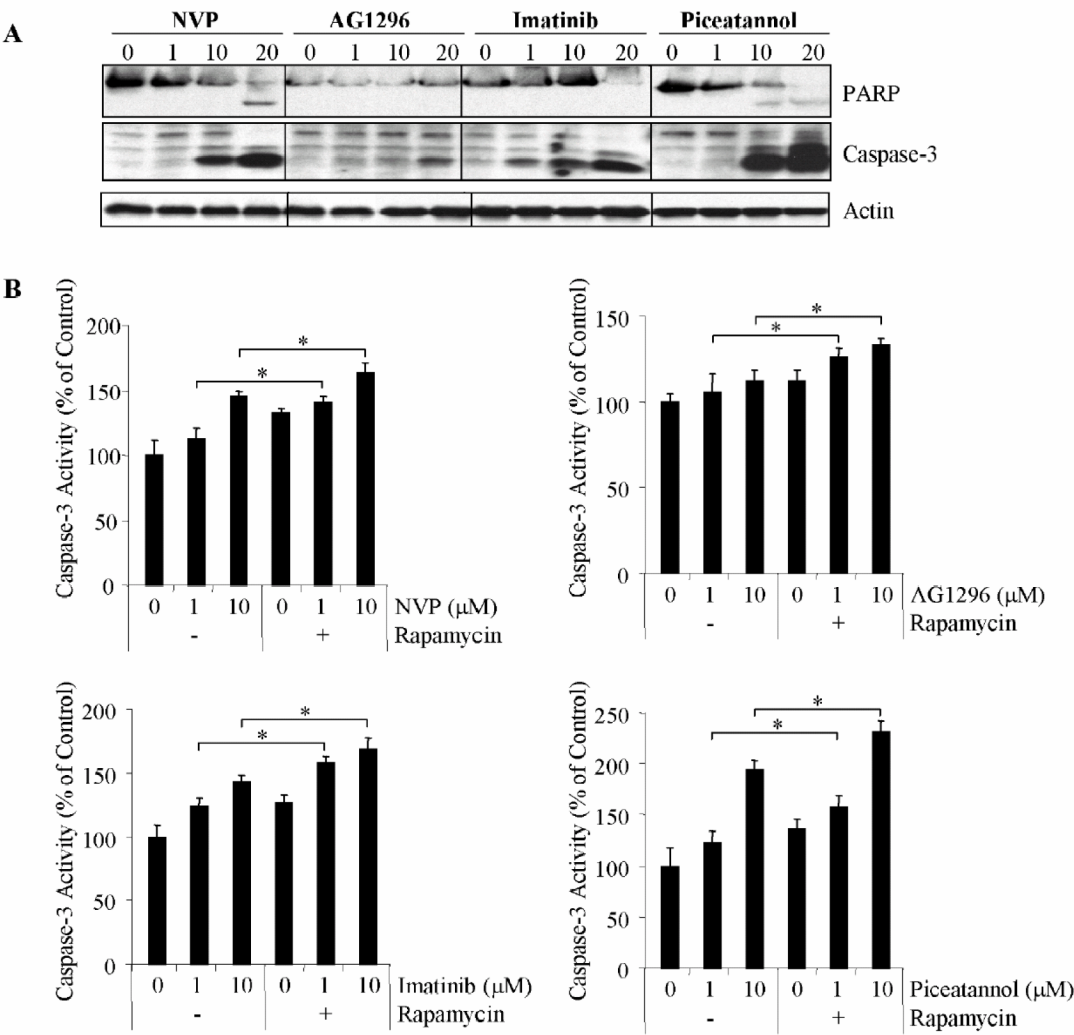


Figure 6



3.5. Novel role for insulin as an autocrine growth factor for malignant brain tumour cells

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Novel role for insulin as an autocrine growth factor for malignant brain tumour cells

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AT/RTs (atypical teratoid/rhabdoid tumours) of the CNS (central nervous system) are childhood malignancies associated with poor survival rates due to resistance to conventional treatments such as chemotherapy. We characterized a panel of human AT/RT and MRT (malignant rhabdoid tumour) cell lines for expression of RTKs (receptor tyrosine kinases) and their involvement in tumour growth and survival. When compared with normal brain tissue, AT/RT cell lines overexpressed the IR (insulin receptor) and the IGFIR (insulin-like growth factor-I receptor). Moreover, insulin was secreted by AT/RT cells grown in serum-free medium. Insulin potently activated Akt (also called protein kinase B) in AT/RT cells, as compared with other growth factors, such as epidermal growth factor. Pharmacological inhibitors, neutralizing antibodies, or RNAi (RNA interference) targeting

the IR impaired the growth of AT/RT cell lines and induced apoptosis. Inhibitors of the PI3K (phosphoinositide 3-kinase)/Akt pathway also impaired basal and insulin-stimulated AT/RT cell proliferation. Experiments using RNAi and isoform-specific pharmacological inhibitors established a key role for the class I_A PI3K p110 α isoform in AT/RT cell growth and insulin signalling. Taken together, our results reveal a novel role for autocrine signalling by insulin and the IR in growth and survival of malignant human CNS tumour cells via the PI3K/Akt pathway.

Key words: Akt, atypical teratoid/rhabdoid tumour (AT/RT), cell proliferation, central nervous system, insulin-like growth factor (IGF), phosphoinositide 3-kinase (PI3K).

INTRODUCTION

The AT/RT (atypical teratoid/rhabdoid tumour) is a highly malignant paediatric tumour of the CNS (central nervous system), which is characterized by unique clinical, biological and histological features [1–4]. Patients with CNS AT/RT respond very poorly to chemotherapy and radiotherapy and thus the prognosis for this particular malignancy is very poor [4–6]. AT/RT is related to other rhabdoid tumours of the kidney [MRT (malignant rhabdoid tumour)] and soft tissues. Most of the rhabdoid tumours harbour inactivating biallelic alterations in the *hSNF5* (Human *SNF5*)/*INI1* gene, a tumour suppressor gene on chromosome 22 [7–9]. *hSNF5/INI1* is a component of the ATP-dependent chromatin remodelling SWI/SNF complex [10]. There are multiple sets of mammalian SWI/SNF complexes, with varying subunit compositions, which play important roles in transcriptional regulation, through both activation and repression of gene transcription [10–12]. Mice with a targeted disruption of the *INI1* gene developed tumours at a high frequency and the resulting tumours displayed loss of expression of the *hSNF5/INI1* protein [13,14]. Deletion of *hSNF5/INI1* was recently reported to cooperate with p53 loss in oncogenic transformation in murine models [15,16]. One of the mechanisms by which *hSNF5/INI1* exerts its tumour suppressor function was shown to involve repression of cyclin D1 gene expression [17]. Targeting cyclin

D1 gene expression was thus suggested to represent a novel therapeutic strategy for AT/RT [17,18].

The insulin/IGF (insulin-like growth factor) family of growth factors are part of an evolutionarily conserved signalling system with a critical role in the growth and development of many tissues as well as the regulation of overall growth and metabolism. This signalling system is characterized by a high complexity and involves multiple proteins including three receptors [IR (insulin receptor), IGFIR (IGF-I receptor) and IGF-II/M-6-PR (mannose 6-phosphate receptor)], three ligands (insulin, IGF-I and IGF-II) and six known types of circulating binding proteins [IGFBP1 (IGF-binding protein 1)–IGFBP6] [19,20]. Both IGF-I and IGF-II bind to the IGFIR, although IGF-I shows a higher affinity than IGF-II [20]. Insulin, the main ligand for the IR, has an IGFIR-binding affinity that is much lower than that of IGF-I [19,20]. The specific receptor for IGF-II, the M-6-PR, differs significantly from the IGFIR, possesses no tyrosine kinase activity and was reported to target IGF-II for lysosomal degradation [21,22]. Signalling by the IGFIR plays a fundamental role in cell growth and malignant transformation and is an important inhibitor of apoptosis [23,24]. The IGFIR is overexpressed in a variety of human tumours including malignant brain tumours [25]. Decreased receptor expression or impaired function was reported to induce a reversal of the transformed phenotype, apoptosis and a decrease in cellular radioresistance and chemoresistance [26]. The IGFIR has thus

Abbreviations used: AT/RT, atypical teratoid/rhabdoid tumour; CNS, central nervous system; Cy3, indocarbocyanine; DMEM, Dulbecco's modified Eagle's medium; DTT, dithiothreitol; EGF, epidermal growth factor; EGFR, EGF receptor; ERK1/2, extracellular-signal-regulated kinase 1/2; FCS, foetal calf serum; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; HA, haemagglutinin; *hSNF5*, human *SNF5*; IGF, insulin-like growth factor; IGFBP1, IGF-binding protein 1; IGFIR, IGF-I receptor; IR, insulin receptor; M-6-PR, mannose 6-phosphate receptor; MRT, malignant rhabdoid tumour; mTOR, mammalian target of rapamycin; MTS, 3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulfophenyl)-2H-tetrazolium; PDX-1, pancreatic duodenal homeobox-1; PI3K, phosphoinositide 3-kinase; PKB, protein kinase B; PTEN, phosphatase and tensin homologue deleted on chromosome 10; RNAi, RNA interference; RTKs, receptor tyrosine kinases; RT, reverse transcriptase; SCF, stem cell factor; shRNA, small-hairpin RNA; siRNAs, small interfering RNAs; S6K, S6 kinase; Tos-Lys-CH₂Cl, tosyl-lysylchloromethane.

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been proposed to be a target for the development of novel anti-cancer therapies [26–29]. In medulloblastoma, targeting of the IGFIR with the inhibitor NVP-AEW541 [30] was recently shown to impair cell growth and survival [31]. In AT/RT cells, a recent report has shown that the IGFIR is involved in anti-apoptotic signalling and contributes to chemoresistance [32]. Less is known about the potential involvement of the related IR in human cancer, although its role has been described in the pathogenesis of certain malignancies [33].

A critical intracellular signalling mediator of the IGFIR is the PI3K (phosphoinositide 3-kinase)/Akt [also called PKB (protein kinase B)] pathway [27,34,35]. Indeed, PI3K signalling is implicated in the control of cell proliferation, survival and motility/metastasis downstream of many different growth factor receptors [35,36]. The importance of PI3K signalling in human cancer is highlighted by the fact that mutations in the tumour suppressor gene *PTEN* (phosphatase and tensin homologue deleted on chromosome 10) occur frequently in human tumours [36,37]. *PTEN* is a phosphatase that antagonizes the action of PI3K by dephosphorylating the D-3 position of polyphosphoinositides [38]. Moreover, previous reports have described activating mutations in the *PIK3CA* gene encoding the catalytic p110 α isoform of class I $_A$ PI3K in a variety of human cancers, including, breast, colon and ovarian cancers, as well as medulloblastoma [39,40].

In the present study, we have investigated the expression pattern and biological functions of components of the IR and IGFIR signalling system in human AT/RT and MRT cell lines. Moreover, we have evaluated the potential of targeting the IR or the IGFIR using RNAi (RNA interference), neutralizing antibodies or the inhibitor NVP-AEW541 [30] as an antiproliferative approach in AT/RT cells. Finally, we have investigated whether targeting downstream signalling mediators of the IR could suppress growth and induce apoptosis in AT/RT cell lines. Our findings describe for the first time a role for autocrine signalling by insulin and the IR in growth and survival of AT/RT cells, which involves the PI3K/Akt pathway.

MATERIALS AND METHODS

Reagents and antibodies

Antibodies against Akt/PKB, caspase 3, HA (haemagglutinin) epitope tag, ERK1/2 (extracellular-signal-regulated kinase 1/2), IGFIR β , INI1, IR β , lamin B, p110 β and p110 δ were obtained from Santa Cruz Biotechnology. Antibodies against activated ERK1/2 (Thr²⁰²/Tyr²⁰⁴), activated Akt (Ser⁴⁷³), and Thr³⁸⁹-phosphorylated S6K (S6 kinase) were from Cell Signaling Technology. The Akt inhibitor [1L-6-hydroxymethyl-chiro-inositol 2-(*R*)-2-*O*-methyl-3-*O*-octadecylcarbonate], IGF-I, the IGFIR neutralizing antibody (clone α IR3), LY294002, rapamycin and PD98059 were from Calbiochem. The anti- β -tubulin antibody and insulin were from Sigma–Aldrich. The IR neutralizing antibody (clone 47-9) was from Biosource. The anti-p85 α antibody was from Upstate Biotechnology. The antibody against p110 α (clone U3A) was a generous gift from Dr A. Klippel (atugen, Berlin, Germany). NVP-AEW541 (Novartis Pharma), YM024, TGX-221 and IC87114 (ICOS Corporation) were dissolved in DMSO at 10 mM and diluted into cell culture medium just prior to use.

Cell lines and cell culture

The human MRT cell lines AS, LP, MON and STM [9] have been described previously. The DAOY medulloblastoma cell line was purchased from the A.T.C.C. (Rockville, MD, U.S.A.). The BT-12 and BT-16 human CNS AT/RT cell lines [32,41] were gifts from

Dr Jaclyn Biegel (The Children's Hospital of Philadelphia, PA, U.S.A.). These cell lines have been established from two infants with CNS AT/RT (BT-12 from a 6-week-old female; BT-16 from a 2-year-old male). They have been analysed for *INI1* mutations by Dr Jaclyn Biegel and both contain *INI1* mutations. Human AT/RT cell lines were grown in DMEM (Dulbecco's modified Eagle's medium; Life Technologies/Invitrogen) with 10% (v/v) FCS (foetal calf serum) and penicillin/streptomycin/L-glutamine, and passaged every 3–5 days by trypsinization. Human MRT cell lines were grown in RPMI 1640 (Life Technologies/Invitrogen) with 10% FCS and penicillin/streptomycin/L-glutamine. For serum-starving, the cells were incubated for 16 h in DMEM containing 0.5% FCS. All cell cultures were maintained at 37°C in a humidified atmosphere with 5% CO₂.

Cell proliferation and apoptosis

AT/RT cell lines (10⁵/ml) were grown in 96-well plates for 3 days in serum (1 or 10%) containing medium in the presence or absence of inhibitors. For growth factor stimulations, cells were incubated in medium containing 1% FCS. Cell proliferation was analysed by MTS [3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulfophenyl)-2H-tetrazolium] assay using the CellTiter 96® Aqueous One Solution Cell Proliferation Assay (Promega).

For detection of apoptosis, AT/RT cells [1 × 10⁶ cells/well in 6-well plates (35 mm)] were incubated for 24 h in the presence or absence of inhibitors. The cells were then washed in 1 × PBS and lysed in 1 × gel-loading buffer [50 mM Tris/HCl, pH 6.8, 2% (w/v) SDS, 100 mM DTT (dithiothreitol), 0.1% (w/v) Bromophenol Blue and 10% (w/v) glycerol]. The samples were denatured for 3 min at 100°C and analysed by SDS/PAGE and Western blot with anti-caspase 3 antibodies.

ELISAs

AT/RT cells were seeded at 5 × 10⁴ cells/well in 6-well plates (35 mm). After 3 h, the cells were washed three times in serum-free medium and incubated in 2 ml of DMEM containing penicillin/streptomycin/L-glutamine. After 5 days, the supernatants were collected, centrifuged to remove cellular contaminants and human insulin was quantified by using the AIA-PACK IRI immunoassay (Tosoh Corporation). The background signal caused by the cell culture medium in the absence of cells was subtracted from the measured values.

Immunofluorescence

AT/RT cells were grown on coverslips and serum-starved for 24 h. The cells were then fixed with 4% (w/v) paraformaldehyde in 1 × PBS and permeabilized with methanol for 10 min at –20°C. The coverslips were blocked with 0.5% (w/v) non-fat dry milk in 1 × PBS for 1 h and incubated with anti-insulin antibody (1:50; Dako) or anti-IR β (1:100; Santa Cruz Biotechnology) for 1 h. The detection was performed using secondary anti-guinea-pig antibody coupled with FITC, or anti-rabbit antibody coupled with Cy3 (indocarbocyanine). Pictures were taken at ×100 magnification with a Zeiss Axioskop fluorescence microscope.

Immunoprecipitations

AT/RT cells grown to confluence on 10 cm dishes were serum-starved and stimulated with growth factors for 10 min at 37°C. After washing with ice-cold 1 × PBS, the cells were lysed for 20 min on ice in 1 ml of lysis buffer [20 mM Hepes/NaOH,

pH 7.4, 150 mM NaCl, 1 % (w/v) Triton X-100, 2 mM EDTA, 10 mM sodium fluoride, 10 % (w/v) glycerol, 1 mM PMSF, 5 mM benzamidine, 1 mM Tos-Lys-CH₂Cl (tosyl-lysylchloromethane), 10 μ M leupeptin, 10 μ M pepstatin A, 2 mM Na₃VO₄ (sodium orthovanadate), 10 mM 2-glycerophosphate and 10 mM NaF]. Immunoprecipitation was performed for 2 h at 4°C with primary antibodies (diluted according to the manufacturer's instructions). Protein G-Sepharose CL-4B (Amersham Biosciences) was then added, and the incubation was continued for 1 h at 4°C. The immunoprecipitates were washed three times in lysis buffer and resuspended in 1× gel-loading buffer. The samples were denatured for 3 min at 100°C and analysed by SDS/PAGE and Western blot.

MS analysis

Samples (10 μ l) were desalted using Millipore C18 ZipTips. An aliquot of 0.5 μ l was applied directly to a prespotted AnchorChip™ target. After 3 min of incubation, 7 μ l of washing solution (0.1 % trifluoroacetic acid) was added on the analyte solution and the whole droplet was removed after a few seconds. MALDI-TOF (matrix-assisted laser-desorption/ionization-time-of-flight) mass spectra were acquired in linear mode using a Bruker Daltonics Autoflex™ mass spectrometer.

RT (reverse transcriptase)-PCR

Total cellular RNA was extracted using the RNeasy Mini kit (Qiagen) according to the manufacturer's instructions. For each RT-PCR, 2 μ g of total RNA was used with the Qiagen One-Step RT-PCR kit. The following primers were used: insulin primer, sense 5'-CGTCCCCGACACTAGGT-3' and antisense 5'-GCAGCCTTTGTGAACCAACAC-3'; IGF-I primer, sense 5'-GTGCTGCTTTGTGATTCTT-3' and antisense 5'-GTCTTGGGCATGTCGGTGTGG-3'; IGF-II primer, sense 5'-ATGGGGAAGTCGATGCTGGTG-3' and antisense 5'-ACGGGTATCTGGGGAAGTTG-3'; PDX-1 (pancreatic duodenal homeobox-1) primer, sense 5'-CTGCGGAGCCGGAGGAGA-AC-3' and antisense 5'-TCTAGAACTACACAGAGAGC-3'; GAPDH (glyceraldehyde-3-phosphate dehydrogenase) primer, sense 5'-GAAGGTGAAGGTGCGAGTC-3' and antisense 5'-GAAGATGGTGATGGGATTTC-3'. The reaction conditions were as follows: reverse transcription at 50°C for 30 min, initial PCR activation at 95°C for 15 min followed by 40 cycles at 95°C for 15 s, 55°C for 20 s and 72°C for 40 s. The PCR products were analysed in 3 % (w/v) agarose gel.

SDS/PAGE and Western-blot analysis

Cellular lysates were prepared with lysis buffer [50 mM Hepes/NaOH, pH 7.4, 150 mM NaCl, 2 mM EDTA, 1 % Triton X-100, 1 % (w/v) deoxycholic acid, 0.1 % SDS, 10 % glycerol, 10 μ M leupeptin, 10 μ M pepstatin A, 1 mM PMSF, 5 mM iodoacetamide, 5 mM benzamidine, 1 mM Tos-Lys-CH₂Cl, 2 mM Na₃VO₄, 10 mM 2-glycerophosphate and 10 mM NaF]. The cells were lysed for 20 min on ice, scraped and lysates were centrifuged at 12000 g for 20 min at 4°C. The supernatants were collected and normalized for protein content by using the BCA (bicinchoninic acid) protein assay kit (Pierce). One volume of 2× gel-loading buffer [100 mM Tris/HCl, pH 6.8, 4 % SDS, 200 mM DTT, 0.2 % (w/v) Bromophenol Blue and 20 % (w/v) glycerol] was then added to the samples, followed by denaturation for 3 min at 100°C and analysed by SDS/PAGE. The gels were transferred on to a hydrophobic PVDF membrane (Hybond-

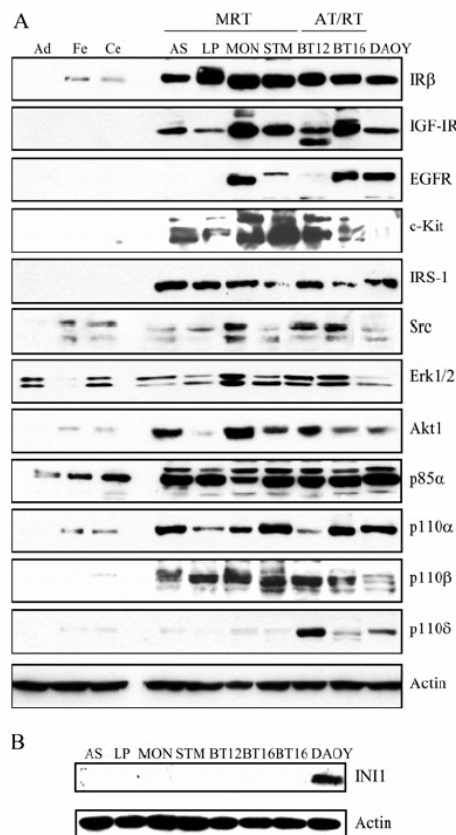


Figure 1 Expression of the IR and its downstream signalling components in MRT and AT/RT cells

(A) Equal amounts of lysates from adult brain (Ad), foetal brain (Fe), foetal cerebellum (Ce), or the cell lines indicated were analysed by Western blot for expression of the proteins indicated. The cell lines analysed were AS, LP, MON, STM (MRT), BT-12, BT-16 (AT/RT) and DAOY (medulloblastoma). (B) Equal amounts of lysates from the cell lines indicated were analysed by Western blot for expression of INI1.

P; Amersham Biosciences) by electrophoresis. The membranes were then blocked in 1× PBS, 5 % (w/v) BSA (phospho-specific antibodies) or 1× PBS/3 % non-fat dry milk (all other antibodies) for 16 h at 4°C. The membranes were incubated with primary antibodies (diluted according to the manufacturer's protocol) for 16 h at 4°C. After washing in 1× PBS and 0.1 % (w/v) Tween 20, the immunoblots were incubated with donkey anti-rabbit IgG or sheep anti-mouse IgG secondary antibodies (1:10000 dilution) coupled with horseradish peroxidase (Amersham Biosciences) for 1 h at room temperature. After washing of the immunoblots, chemiluminescence was used for detection, using the ECL® (enhanced chemiluminescence) Western blotting detection reagents (Amersham Biosciences) according to the manufacturer's protocol.

Transient and stable transfections in AT/RT cells

Human AT/RT cells were transiently transfected with Akt/PKB constructs in pUSE (Upstate Biotechnology), or with PI3K shRNA (small-hairpin RNA) constructs in pRETRO-SUPER [42] by using Lipofectamine™ 2000 (Invitrogen). The transfections

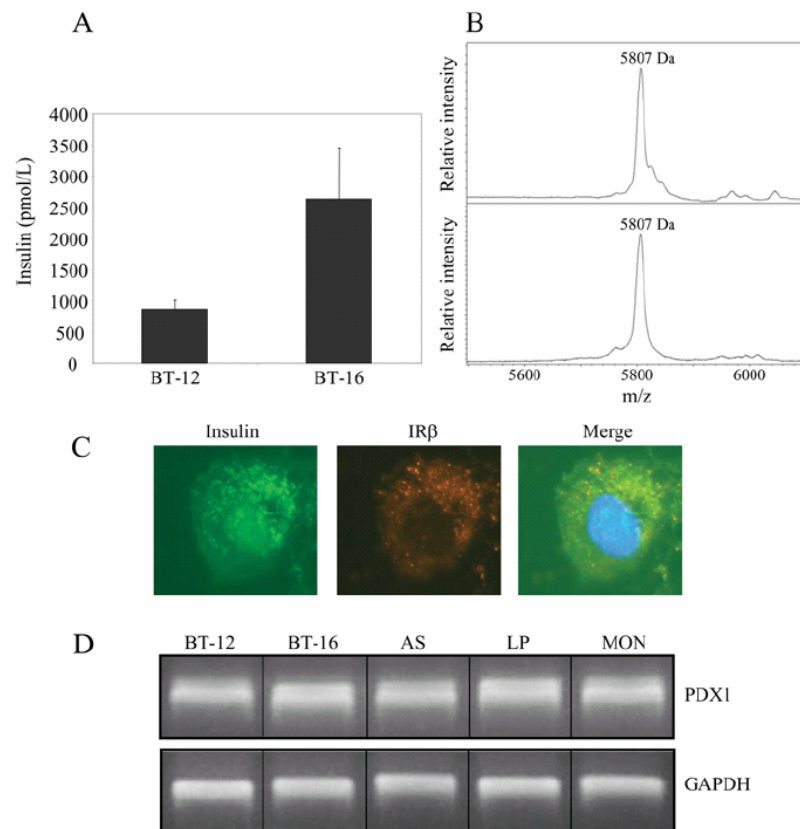


Figure 2 Human AT/RT cells secrete insulin under serum-free conditions

(A) Serum-free supernatants from AT/RT cells were analysed after 5 days in culture by ELISA to detect insulin production. Results are the means with S.D. from a representative experiment (out of three) performed in triplicate. (B) Serum-free supernatants from BT-16 cells (upper panel) or purified recombinant human insulin (lower panel) were analysed by MS. (C) Expression of insulin (left) and the IRβ (centre) in BT-16 cells was investigated by immunofluorescence ($\times 100$ magnification). The detection was performed using secondary antibodies coupled with FITC (insulin) or Cy3 (IRβ). The right panel shows the merged pictures and the cell nucleus stained with DAPI (4',6-diamidino-2-phenylindole). (D) The expression of PDX-1 was detected in MRT and AT/RT cells using RT-PCR. GAPDH expression was analysed in parallel as a loading control.

were performed in 96-well plates (MTS assays) or 6-well plates (Western-blot analysis), using the amounts of DNA and LipofectamineTM 2000 recommended by the manufacturer's protocol. Opti-MEM I medium (Invitrogen) was used for the transfection and replaced by growth medium after 24 h.

The siRNAs (small interfering RNAs) targeting the IRβ and IGFIRβ and non-targeting control siRNA were purchased from Dharmacon. The siRNAs were transfected into BT-12 or BT-16 cells using LipofectamineTM 2000 (Invitrogen). The transfections were performed in 96-well plates (MTS assays) or 6-well plates (Western-blot analysis), using the amounts of siRNA and LipofectamineTM 2000 recommended by the manufacturer's protocol. Opti-MEM I medium (Invitrogen) was used for the transfection and replaced by growth medium after 24 h. Cell responses were assessed 72 h post-transfection.

For stable expression BT-16 cells (in 10 cm dishes) were transfected with an HA-tagged INI1 construct in pcDNA3 (Invitrogen) or with empty vector using LipofectamineTM (Invitrogen). The amounts of DNA and LipofectamineTM used were as recommended by the manufacturer's protocol. After 48 h, the cells were diluted 1:10 in growth medium containing G418 (1.0 mg/ml). A population of resistant cells was expanded and analysed after

selection. Western-blot analysis was used to confirm expression of HA-tagged INI1.

RESULTS

Expression of components of the IR and IGFIR signalling pathways in AT/RT cells

We characterized a panel of established human AT/RT cell lines (BT-12 and BT-16) [32,41], MRT lines (AS, LP, MON and STM) [9] and medulloblastoma (DAOY) for expression of RTKs (receptor tyrosine kinases) to study further their involvement in tumour cell proliferation and survival. Lysates from normal adult brain, foetal brain and foetal cerebellum were analysed in parallel as controls. Western-blot analysis revealed that MRT and AT/RT cell lines overexpressed the IR and IGFIR, as compared with the normal brain samples (Figure 1A). Expression of the EGFR [EGF (epidermal growth factor) receptor], ErbB2 and c-Kit were also detected in the panel of cell lines (Figure 1A and results not shown). In contrast, the PDGFR (platelet-derived growth factor receptor) was not detected in the cell lines under study (results not shown). The expression of components of the PI3K/Akt signalling pathway in the panel of MRT and AT/RT cell lines was then

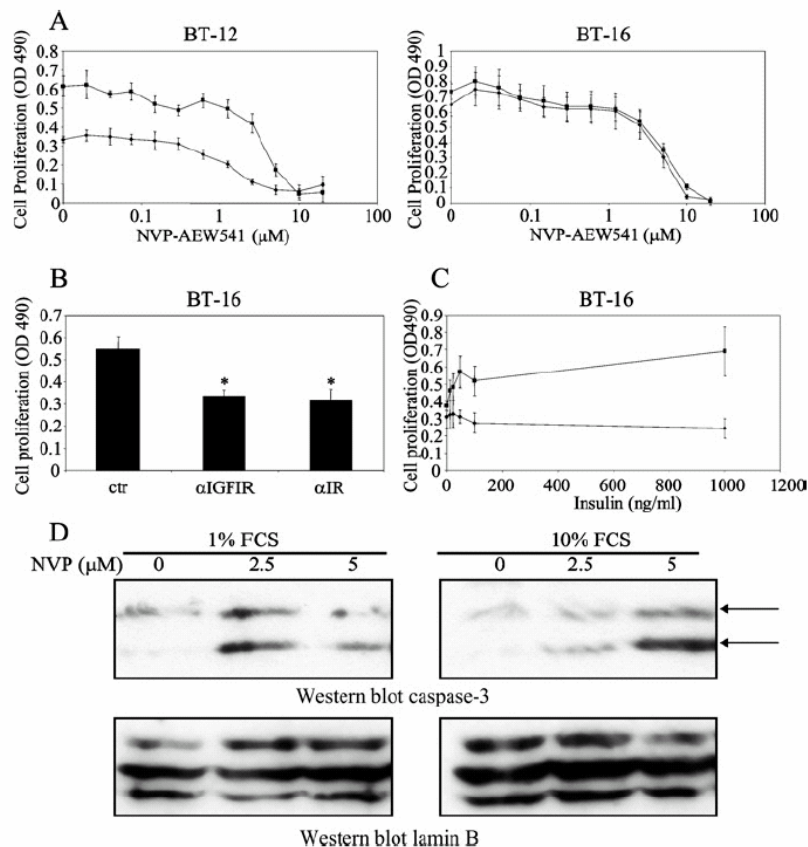


Figure 3 A pharmacological inhibitor or a neutralizing antibody targeting the IR impairs AT/RT cell proliferation

(A) AT/RT cells were incubated in the presence of increasing concentrations of the inhibitor NVP-AEW541 in a medium containing 10% (squares) or 0.5% (diamonds) FCS. Cell proliferation was determined after 72 h. Results are the means with S.D. from a representative experiment (out of three) performed with eight repetitions. (B) BT-16 cells were incubated in serum-free medium in the presence of neutralizing antibodies targeting either the IGFIR or the IR (10 $\mu\text{g/ml}$) and cell proliferation measured after 72 h. Results are the means with S.D. from three experiments performed in quadruplicate (*, $P < 0.05$ by ANOVA test). (C) BT-16 cells were incubated with increasing concentrations of insulin in serum-free medium in the presence of LY294002 (10 μM , diamonds) or vehicle (squares). Cell proliferation was measured after 72 h. Results are the means with S.D. from a representative experiment (out of three) performed with eight repetitions. (D) BT-12 cells were incubated for 20 h in the presence of increasing concentrations of the inhibitor NVP-AEW541 and the induction of apoptosis assessed by Western blot for the active fragments of caspase 3 (20 and 17 kDa, arrows). The blots were reprobed for lamin B as a loading control.

investigated. All cell lines expressed the PI3K regulatory subunit p85 α and the p110 α and p110 β catalytic subunits (Figure 1A). In addition, both AT/RT cell lines overexpressed the p110 δ isoform (Figure 1A). MRT and AT/RT cell lines displayed comparable levels of IRS-1 (IR substrate-1), mTOR (mammalian target of rapamycin) and ERK1/2 (Figure 1A and results not shown). The AT/RT and MRT cell lines did not express INI1, in contrast with DAOY medulloblastoma cells, as expected (Figure 1B). Indeed, AT/RT and MRT cell lines and tumours harbour inactivating biallelic alterations in the *hSNF5/INI1* gene, leading to loss of expression of the INI1 protein [1,9]. In contrast, these mutations are not found in medulloblastoma [43].

Human AT/RT secrete insulin in an autocrine manner

We next investigated whether AT/RT cells produced growth factors in an autocrine fashion. An ELISA revealed that both BT-12 and BT-16 cell lines secreted insulin into the growth medium, when cultivated under serum-free conditions (Figure 2A). The BT-16 cell line appeared to produce higher amounts of insulin than

BT-12 (2628 pmol/l versus 867 pmol/l). IGF-I or IGF-II secretion could not be detected in either BT-12 or BT-16 cells grown in serum-free medium (results not shown). However, an RT-PCR analysis revealed that IGF-I mRNA was expressed in BT-16 cells, while IGF-II expression was detectable in BT-12 cells (see Supplementary Figure 1 at <http://www.BiochemJ.org/bj/406/bj4060057add.htm>). To confirm that the growth factor secreted by BT-16 cells corresponded to human insulin, supernatants of BT-16 cells were analysed by MS. MS analysis revealed the presence of a protein of 5807 Da, corresponding to human insulin in serum-free supernatants obtained from BT-16 cells (Figure 2B). Immunofluorescence analysis revealed that individual BT-16 cells co-expressed insulin and the IR, indicating the presence of an autocrine signalling loop in these cells (Figure 2C). We next performed RT-PCR analysis to investigate the expression of the transcription factor PDX-1 in the panel of cell lines. PDX-1 is a master regulator of pancreas development and β -cell function, which participates in the transcription of several genes, including *insulin* [44]. This analysis revealed strong expression of PDX-1 mRNA in the BT-12, BT-16 and MRT cell lines, confirming their

insulin-producing phenotype (Figure 2D). We next investigated whether other human cancer cell lines also secrete insulin under similar culture conditions. However, an analysis of a panel of human medulloblastoma and neuroblastoma cell lines failed to document insulin secretion under serum-free culture conditions (results not shown), indicating that the response is selective for CNS AT/RT cells.

Inhibition of AT/RT cell proliferation by targeting the IR

The specific IGFIR/IR kinase inhibitor NVP-AEW541 [30] inhibited proliferation of BT-12 and BT-16 cell lines (Figure 3A), in a dose-dependent manner with IC_{50} values of 2 μ M in BT-12 and 5 μ M in BT-16 cells (Figure 3A). In BT-12 cells, NVP-AEW541 was effective at slightly lower concentrations, when cells were incubated in medium containing low serum, as compared with high serum (Figure 3A). In contrast, no differences in sensitivities were observed in the BT-16 cell line (Figure 3A). To confirm these observations, cell proliferation of BT-12 or BT-16 cells was assessed in the presence of neutralizing antibodies specific either for the IGFIR or for the IR. Proliferation of BT-16 cells in serum-free medium was significantly inhibited by the anti-IR neutralizing antibody (Figure 3B). A similar effect was observed with the anti-IGFIR neutralizing antibody (Figure 3B). The anti-IR neutralizing antibody also significantly inhibited proliferation of BT-12 and BT-16 cells in serum-containing medium (results not shown). Increasing concentrations of insulin stimulated proliferation of BT-16 cells in serum-free medium (Figure 3C) and the response was completely inhibited by a pharmacological PI3K inhibitor (LY294002), indicating that PI3K is essential for insulin-stimulated cellular responses in AT/RT cells. The maximal increase in cell proliferation was observed at an insulin concentration of 50 ng/ml (8.6 nM) and concentrations up to 1000 ng/ml had no significantly higher effect (Figure 3C). Inhibiting IGFIR/IR function with NVP-AEW541 also induced apoptosis in AT/RT cells, as assessed by caspase 3 activation (Figure 3D), indicating that the autocrine signalling loop involving the IR contributes to cell survival.

An RNAi approach was used to confirm the critical role of the IR and IGFIR in supporting AT/RT cell growth and survival. Transfection of BT-12 and BT-16 cells with siRNA targeting either the IR β or the IGFIR β resulted in a significant decrease in cell viability (Figures 4A and 4B and results not shown). To verify the specificity of the effect of the siRNA targeting the IR β , protein down-regulation was assessed by Western-blot analysis in BT-12 and BT-16 cells (Figure 4C and results not shown).

Activation of the PI3K/Akt signalling pathway by insulin in AT/RT cells

The ability of polypeptide growth factors to activate PI3K/Akt, ERK1/2 and ribosomal protein S6K was then investigated in BT-12 and BT-16 cells. Insulin most potently activated Akt, as compared with EGF and SCF (stem cell factor), whereas activation of ERK1/2 was comparable between all growth factors (Figure 5A). The IGFIR/IR kinase inhibitor NVP-AEW541 (2.5 μ M) completely inhibited IGF-I- and insulin-activated responses (Figure 5B). Autophosphorylation of the IR was also detected in insulin-stimulated AT/RT cells, confirming the specificity of the responses observed (Figure 5C).

Our data so far had revealed activation of the PI3K/Akt, S6K and ERK1/2 pathways in AT/RT cells stimulated by polypeptide growth factors. Therefore we next investigated the contributions of these pathways to proliferation in BT-12 and BT-16 cells.

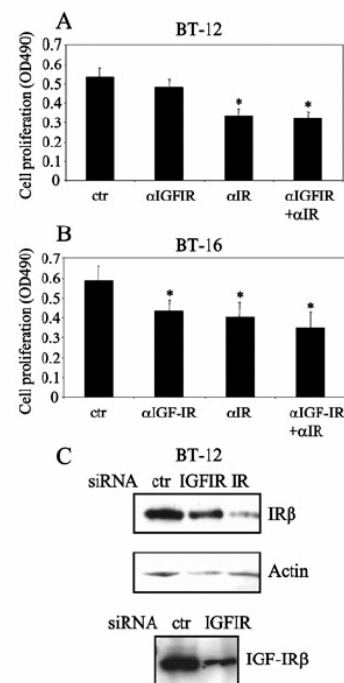


Figure 4 Down-regulation of IR by siRNA treatment impairs AT/RT cell proliferation

(A, B) BT-12 or BT-16 AT/RT cells were transiently transfected with non-targeting siRNA (ctr), or siRNA targeting the IGFIR or the IR, alone or in combination, where indicated. Cell proliferation was measured after 72 h. Results are the means with S.D. from three experiments performed in quadruplicate (*, $P < 0.05$ by ANOVA test). (C) BT-12 AT/RT cells were transiently transfected with siRNAs as indicated and expression of the IR β and IGFIR β was analysed by Western blot after 72 h.

Cell proliferation was assessed in the presence of the PI3K inhibitor LY294002, rapamycin, the MEK [MAPK (mitogen-activated protein kinase)/ERK kinase] inhibitor PD98059, or a pharmacological Akt/PKB inhibitor. AT/RT cell proliferation was significantly impaired by LY294002 or rapamycin, in both BT-12 and BT-16 cells grown in low (1%) or high (10%) serum (Figure 5D). The Akt inhibitor completely inhibited proliferation of the BT-12 cell line in low, but not high serum, while having a lesser effect in the BT-16 cell line (Figure 5D). To confirm the involvement of PI3K/Akt signalling in AT/RT cell proliferation, a dominant-negative catalytically inactive Akt (AktDN) construct was transiently transfected into BT-12 and BT-16 cells. Western-blot analysis confirmed expression of the construct in AT/RT cells (results not shown). The AktDN construct significantly inhibited proliferation in both cell lines (Figure 5E). In contrast, transfection of an activated Akt mutant (myrAktCA) had no significant effect on AT/RT cell proliferation.

The class I α PI3K isoform p110 α controls AT/RT cell proliferation and insulin-stimulated Akt activation

To confirm the involvement of PI3K signalling in AT/RT cell responses to insulin, a panel of isoform-specific class I α PI3K inhibitors was tested in AT/RT cells. The pharmacological p110 α inhibitor YM024 [45] inhibited proliferation of AT/RT cells in a dose-dependent manner with an IC_{50} of 1.5 μ M (Figure 6A). In contrast, the p110 β inhibitor TGX-221 [46] and the p110 δ

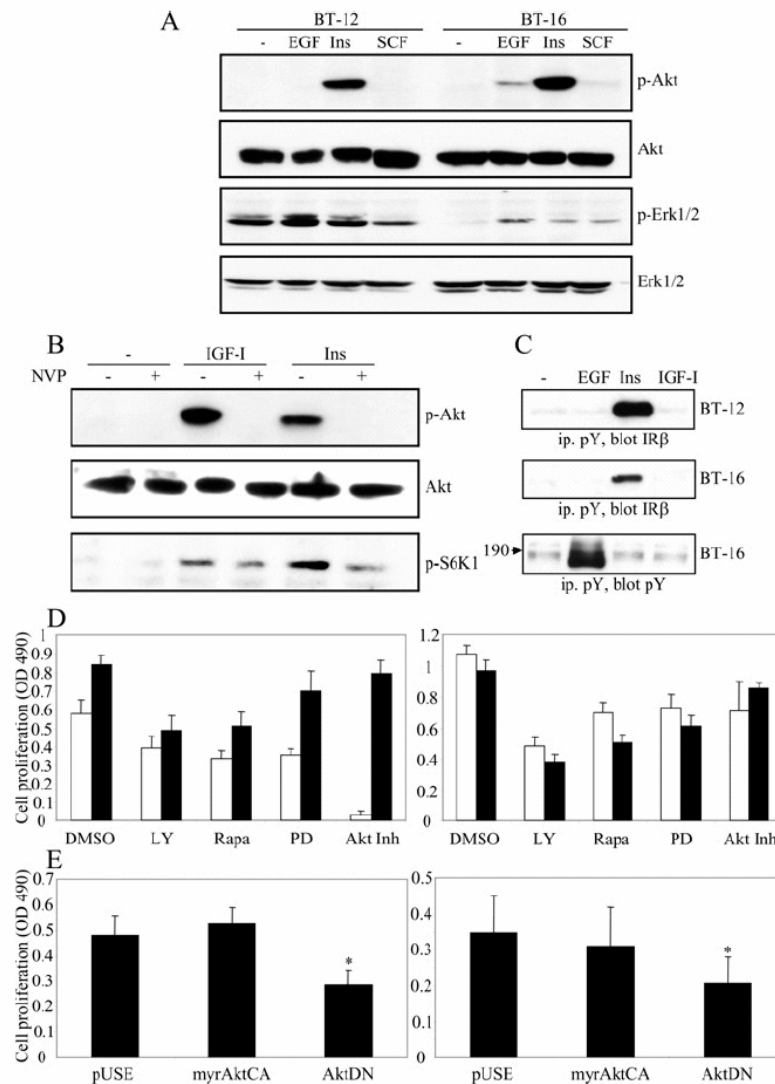


Figure 5 Insulin activates the PI3K/Akt pathway in AT/RT cells

(A) Serum-starved AT/RT cells were stimulated with growth factors where indicated (40 ng/ml EGF; 50 ng/ml Ins; 20 ng/ml SCF) for 10 min, and activation of Akt and ERK was determined by Western blot with phospho-specific antibodies. Abbreviations: p-Akt, Ser⁴⁷³-phosphorylated Akt; p-ERK, Thr²⁰²/Tyr²⁰⁴-phosphorylated ERK. (B) Serum-starved BT-16 cells were pretreated with NVP-AEW541 (2.5 μ M), stimulated with the growth factors indicated (50 ng/ml) for 10 min and activation of Akt and S6K1 was determined as above. Abbreviation: p-S6K1, Thr³⁹⁹-phosphorylated S6K. (C) Serum-starved AT/RT cells were stimulated with the growth factors indicated (10 min) and anti-phosphotyrosine (pY) immunoprecipitates were analysed by Western blots for the relevant receptors. (D) BT-12 (left panel) or BT-16 (right panel) cells were incubated in a medium containing 10% (closed bars) or 0.5% (open bars) FCS in the presence of the inhibitors indicated [LY294002 10 μ M (LY); rapamycin 20 ng/ml (Rapa); PD98059 25 μ M (PD); Akt inhibitor 20 μ M (Akt Inh)], or vehicle (DMSO). Cell proliferation was determined after 72 h. Results are the means with S.D. from a representative experiment (out of three) performed with eight repetitions. (E) BT-12 (left panel) or BT-16 (right panel) cells were transiently transfected with empty vector, or constructs encoding activated (myrAktCA) or dominant-negative Akt (AktDN). Cell proliferation was determined after 72 h. Results are the means with S.D. from three experiments performed in quadruplicate (*, $P < 0.05$ by ANOVA test).

inhibitor IC87114 [47] had a less pronounced effect on AT/RT cell proliferation (Figure 6A). The pharmacological p110 α inhibitor YM024 also inhibited insulin-stimulated Akt activation, whereas TGX-221 and IC87114 did not impair the response (Figure 6B and results not shown). shRNA constructs targeting the catalytic subunits of class I α PI3Ks were then transiently transfected into BT-16 cells to investigate their impact on cell proliferation. Western-blot analysis confirmed down-regulation of the expression of the target genes by the relevant shRNA construct

(Figure 6D). The shRNA constructs targeting *PIK3CA* (encoding p110 α) strongly (>80%) inhibited BT-16 cell proliferation (Figure 6C). In contrast, RNAi targeting of *PIK3CB* resulted in no significant effect on AT/RT cell proliferation (Figure 6C). Moreover, insulin-stimulated Akt activation was abrogated by transfection of BT-16 cells with the shRNA construct targeting *PIK3CA* (results not shown). Thus the p110 α isoform appears to play a crucial role in controlling AT/RT cell proliferation and insulin-stimulated Akt activation.

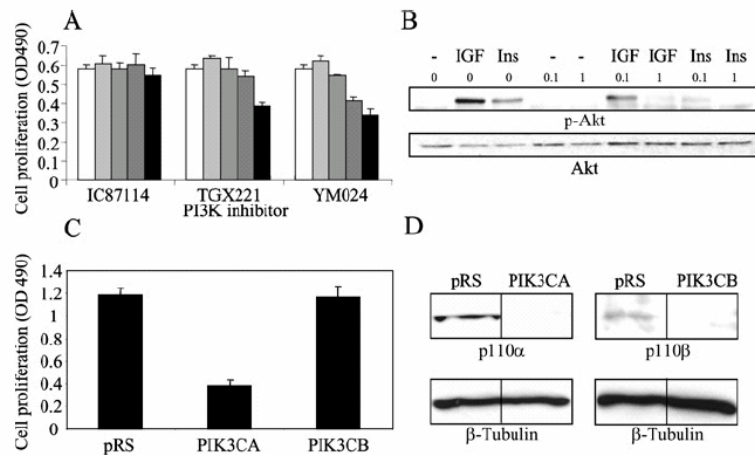


Figure 6 The PI3K p110 α isoform controls AT/RT cell proliferation and insulin signalling

(A) BT-16 cells were incubated with increasing concentrations of isoform-specific PI3K inhibitors [0.01 μ M (light grey bars), 0.1 μ M (medium grey bars), 1 μ M (dark grey bars), 10 μ M (closed bars) or vehicle (open bars)]. Cell proliferation was determined after 72 h. Results are the means with S.D. from a representative experiment (out of three) performed in quadruplicate. (B) Serum-starved BT-16 cells were pre-incubated with the p110 α inhibitor YM024 (micromolar concentrations) and stimulated with growth factors (50 ng/ml insulin; 50 ng/ml IGF-I) where indicated for 10 min. Akt activation was determined by Western blot with phospho-specific antibodies. Abbreviation: p-Akt, Ser⁴⁷³-phosphorylated Akt. (C, D) BT-16 cells were transiently transfected with shRNA constructs targeting PI3K isoforms (PIK3CA: p110 α ; PIK3CB: p110 β) or empty vector (pRS). (C) Cell proliferation was assessed after 72 h. Results are the means with S.D. from a representative experiment (out of three) performed with eight repetitions. (D) Protein down-regulation was determined by Western-blot analysis.

Ectopic expression of INI1 does not affect the IR signalling pathway in AT/RT cells

Since AT/RT cells frequently display mutations in the *INI1* gene, we investigated the impact of ectopic re-expression of the protein in BT-16 cells. BT-16 stably transfected with an *INI1* expression vector displayed reduced proliferation under either low- or high-serum culture conditions (Figure 7A). However, BT-16 transfected with *INI1* still displayed detectable insulin mRNA expression (Figure 7C). Moreover, the expression levels of the IR and IGFIR were not affected, as assessed by Western-blot analysis (Figure 7D). These results indicate that the establishment of the autocrine loop involving insulin and its receptor is independent of *INI1* loss in AT/RT cells.

DISCUSSION

Molecular abnormalities linked with human AT/RT include germline and somatic mutations in the *INI1* gene that encodes a chromatin remodelling factor and has been suggested to function as a tumour suppressor [7–9]. A recent report has also documented epigenetic repression of the *RASSF1* (Ras association domain family 1) gene in AT/RT cell lines and primary tumours [41]. RTK signalling has not yet been studied in detail in AT/RT cells. Expression of the IGFIR and IGF-II was reported in a limited number of cases of AT/RT tumours [25,48]. Targeting the IGFIR with antisense oligonucleotides resulted in increased apoptosis and sensitivity to the chemotherapeutic agents cisplatin and doxorubicin in AT/RT cells [32]. In the case of the MRTs, the EGFR inhibitor gefitinib was reported to have anti-tumour effects *in vitro* and *in vivo* [49]. Moreover, the PI3K/Akt pathway was reported to be involved in the resistance of MRT cells to chemotherapy and radiotherapy [50].

We have characterized a panel of human MRT and AT/RT cell lines for expression of RTKs and their downstream signalling mediators, in order to study the potential of targeting these molecules to inhibit cell proliferation and survival. The IR and

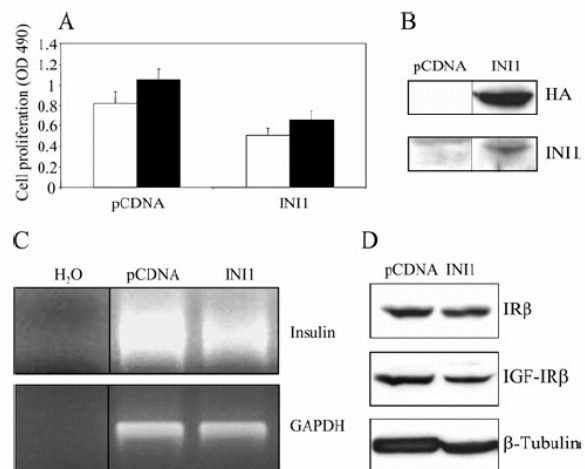


Figure 7 Ectopic expression of *INI1* reduces the proliferation of AT/RT cells, without effect on IR expression

(A) BT-16 cells were stably transfected with empty vector (pCDNA) or HA-tagged *INI1*. Cell proliferation in a medium containing 0.5% (open bars) or 10% (closed bars) FCS was determined after 72 h. Results are the means with S.D. from a representative experiment (out of three) performed with eight repetitions. (B) Expression of HA-tagged *INI1* in the transfected BT-16 cells was verified by Western-blot analysis. (C) Insulin mRNA expression in BT-16 cells transfected with empty vector (pCDNA) or HA-tagged *INI1* was determined by RT-PCR. GAPDH was analysed in parallel as a control. (D) The expression of the IR β and the IGFIR β in BT-16 cells transfected with empty vector (pCDNA) or HA-tagged *INI1* was determined by Western blot.

IGFIR were found overexpressed in both AT/RT and MRT cell lines, as compared with normal brain tissue. Moreover and surprisingly, AT/RT cell lines secreted insulin when grown under serum-free conditions, indicating autocrine signalling events. To our knowledge these AT/RT cell lines are the first example of human CNS tumour cell lines secreting insulin. Moreover, the

only other examples of insulin secretion by cells other than pancreatic β -cells are sperm cells [51]. The concentration of insulin measured in supernatants from BT-16 cells was 2.5 nM, which is in the biological range. Maximal biological responsiveness to insulin tends to occur at concentrations in the range 10–20 nM [52–54] and insulin had maximal effects on BT-16 cell proliferation at a concentration of 8.6 nM. It is conceivable that AT/RT cells also produce other growth factors in an autocrine fashion. Indeed, IGF-I and IGF-II were detected at the mRNA level in BT-16 and BT-12 cells respectively, as recently reported [32]. We were unable to detect free IGF-I and IGF-II in supernatants from AT/RT cells by ELISA, but this could be due to the fact that IGFs were bound to IGF-binding proteins. Autocrine signalling by IGF-I via the IGFIR in BT-16 cells would explain the inhibitory effects of IGFIR-neutralizing antibodies or siRNA on the proliferation of these cells.

Insulin activated PI3K/Akt, S6K and ERK signalling, whereas other growth factors such as EGF or SCF selectively activated some, but not all of the pathways. Targeting the IGFIR kinase activity with NVP-AEW541 resulted in inhibition of AT/RT proliferation, although at higher IC₅₀ values than reported in other tumour cells [30]. These increased IC₅₀ values possibly reflect co-expression of the IR and IGFIR in AT/RT cell lines, since the IC₅₀ of NVP-AEW541 for the IR was reported to be 2.3 μ M in cells [30,55]. This model was supported by the observations that neutralizing antibodies or siRNA targeting the IR β inhibited the proliferation of AT/RT cells. Consequently, our results demonstrate that insulin secreted by AT/RT cells in an autocrine fashion activates the IR and thus contributes to AT/RT cell proliferation and survival. This mechanism of IR activation appears to be different from the previously reported activation loop involving IGF-II and the IR isoform A in human cancer cells [56–58]. The molecular mechanisms underlying the establishment of the autocrine insulin signalling loop in AT/RT cells are currently unclear. Loss of *hSNF5/IN1* did not appear to be a major cause of the expression of insulin and the IR by AT/RT cells, since transfection of IN1 did not substantially alter the expression of these molecules. Intriguingly, the pancreatic transcription factor PDX-1 was detected in AT/RT and MRT cells, indicating that aberrant expression of transcription factors may drive these cancer cells towards an insulin-producing phenotype. A recent survey of mutations in human tumour genomes has revealed frequent mutations in transcription factors, emphasizing the contribution of abnormalities in transcription to the development of human cancer [59].

To investigate whether targeting downstream signalling mediators of the IR could provide a means of inhibiting proliferation of AT/RT cells, we used a combination of pharmacological and RNAi approaches. This revealed that the PI3K/Akt/mTOR pathway was crucial in the control of AT/RT cell proliferation. Moreover, a selective role for the PI3K isoform p110 α in transducing signals from the IR was uncovered in AT/RT cells, in good agreement with recent reports documenting the crucial role of p110 α in insulin signalling [60,61]. Thus pharmacological inhibitors targeting the PI3K p110 α isoform may have antiproliferative potential in human cancer cells where this isoform is activated by the IR.

Insulin has various biological effects in a broad range of tissues, and its functions in the brain include neuronal survival and regulation of energy homeostasis [62]. Although a large body of evidence exists implicating IGF-I and IGF-II as autocrine growth factors in a broad range of human malignancies [24,27], such a function has not yet been described for insulin in CNS tumours. In the light of the novel function for insulin as an autocrine growth factor for CNS AT/RT cells, further studies are warranted to uncover its potential role in other human cancers.

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3.6. Targeting the phosphoinositide 3-kinase isoform p110 δ impairs growth and survival in neuroblastoma cells
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Targeting the phosphoinositide 3-kinase isoform p110 δ impairs growth and survival in neuroblastoma cells

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Running title: Role of p110 δ in neuroblastoma

Keywords: neuroblastoma; phosphoinositide 3-kinase; Akt; mTOR; S6K

Abstract

Purpose: The phosphoinositide 3-kinase (PI3K)/Akt pathway is frequently activated in human cancer and plays a crucial role in neuroblastoma biology. We were interested in gaining further insight into the potential of targeting PI3K/Akt signalling as a novel anti-proliferative approach in neuroblastoma.

Experimental Design: The expression pattern and functions of class I_A PI3K isoforms were investigated in tumor samples and cell lines. Effects on cell survival and downstream signalling were analysed following down-regulation of p110 α or p110 δ in SH-SY5Y and LAN-1 cells by means of RNA interference (RNAi).

Results: Over-expression of the catalytic p110 δ and regulatory p85 α isoforms was detected in a panel of primary neuroblastoma samples and cell lines, as compared to normal adrenal gland tissue. While down-regulation of either p110 α or p110 δ led to impaired cell growth, reduced expression of p110 δ also had a selective effect on the survival of SH-SY5Y cells. Decreased levels of p110 δ were found to induce apoptosis and lead to lower expression levels of anti-apoptotic Bcl-2 family proteins. SH-SY5Y cells with decreased p110 δ levels also displayed reduced activation of ribosomal protein S6 kinase (S6K) in response to stimulation with epidermal growth factor (EGF) and insulin-like growth factor-1 (IGF-1).

Conclusions: Together, our data reveal a novel function of p110 δ in neuroblastoma growth and survival.

Introduction

Neuroblastoma is the most common extra cranial solid tumor occurring in children and accounts for 8% to 10% of all paediatric malignancies (1, 2). High-risk disease, present in about half of the patients, is characterised by unresectable primary lesions and metastasis (2). Treatment of high-risk neuroblastoma with high-dose chemotherapy including peripheral stem cell rescue and radiotherapy resulted only in 34% three-year event-free survival probability (3).

A better understanding of the biology of neuroblastoma will potentially lead to the identification of novel therapeutic targets, which in turn could facilitate the development of new drugs for neuroblastoma. A promising field of investigation is to target receptor tyrosine kinase (RTK) signalling to some of their downstream mediators such as phosphoinositide 3-kinase (PI3K), Akt and the mammalian target of rapamycin (mTOR). Polypeptide growth factors have indeed been shown to play a key role in neuroblastoma biology. Insulin-like growth factor (IGF) signalling has been extensively studied in the context of neuroblastoma proliferation, survival and motility (4-7). Several potential anti-tumor approaches involving the IGF-1 system have been reported in neuroblastoma (8, 9). Moreover, inhibition of platelet-derived growth factor receptor (PDGFR) and c-Kit signalling with imatinib mesylate was reported to impair growth in neuroblastoma cell lines (10). Neurotrophins such as brain-derived neurotrophic factor (BDNF) also play an important role in neuroblastoma chemoresistance by binding to the Trk receptor family (11).

In view of the fact that neuroblastoma express a variety of different RTKs, it remains unclear whether targeting individual receptors will provide a successful therapeutic strategy. An alternative approach would be to identify downstream signalling molecules essential for transmitting the proliferative and survival message of several different RTKs. Phosphoinositide 3-kinase (PI3K) represents such a molecule, in view of its crucial role in controlling cell proliferation, survival and motility/metastasis downstream of many different RTKs (12-14). PI3Ks are an enzyme family comprising eight catalytic isoforms in humans, with different substrate specificities, regulatory mechanisms and tissue distribution (12, 14). The importance of PI3K signalling in human cancer was first demonstrated by the observation that mutations in the tumor suppressor gene *PTEN* occur frequently in human tumours. PTEN is a phosphatase that antagonises the action of PI3K by dephosphorylating the D-3 position of polyphosphoinositides (14, 15). Moreover, recent reports have described activating mutations

in the *PIK3CA* gene encoding the catalytic p110 α isoform of PI3K in a variety of human cancers, including breast, colon and ovarian cancer, as well as medulloblastoma (16). In neuroblastoma, brain-derived neurotrophic factor (BDNF) was shown to protect the tumor cells from chemotherapy-induced apoptosis via the PI3K pathway (17). IGF-1 signalling via PI3K was shown to be required for neuroblastoma differentiation, cytoskeletal rearrangements (18), as well as angiogenesis and vascular endothelial growth factor (VEGF) expression (19). PI3K signalling is also activated by epidermal growth factor (EGF) in neuroblastoma cells and contributes to cell proliferation by this growth factor (20). Thus, targeting the PI3K/Akt/mTOR/S6K pathway may represent an attractive novel approach to develop therapies for neuroblastoma.

In the present report we have evaluated the expression of PI3K isoforms in primary human neuroblastoma samples and cell lines. Moreover, we have investigated whether targeting distinct PI3K isoforms could impair growth and survival of neuroblastoma cell lines. Our results show for the first time that the class I_A PI3K p110 δ is over-expressed in a subset of neuroblastoma samples and plays a crucial role in the growth and survival of neuroblastoma cells.

Materials and methods

Reagents and Antibodies. Antibodies were purchased from the following companies: p85 α , p110 β , p110 δ , PARP, PTEN, Akt/PKB, Erk1/2, Santa Cruz Biotechnology; S6 protein, 4EBP1 and phosphospecific antibodies for Akt/PKB (Ser473; Thr308), Erk1/2 (Thr202/Tyr204), S6 protein (Ser235/236; Ser240/244), 4E-BP1 (Thr37/46), Cell Signaling Technology; β -Actin, Sigma-Aldrich; p110 α (clone U3A), generous gift from Dr. A. Klippel. Analysis of proteins involved in apoptosis was performed using the Pro-Survival and the Pro-Apoptosis Bcl-2 Family Antibody Sampler Kit (Cell Signaling). LY294002, rapamycin, EGF, PDGF and IGF-1 were obtained from Calbiochem.

Determination of PI3K-related gene expression in human primary neuroblastoma samples by cDNA microarray analysis. Expression of PI3K-related genes was determined in tumours from 68 neuroblastoma patients by Affymetrix U95A array analysis. The patient cohort and data normalisation procedures have been described elsewhere (21). Correlation of PI3K-related gene expression with molecular and clinical parameters was determined using the stats package included in R2.2 (www.r-project.org). Visualisation of gene expression was accomplished using Spotfire 8.1.

Primary neuroblastoma samples. Ethical approval to use residual tissue was obtained. RNAlater-preserved tumor tissue was available from the Swiss Paediatric Oncology Group tumor bank from neuroblastoma patients diagnosed between January 2003 and December 2005 at the University Children's Hospital of Zurich, (n=14), the Children's Hospital Luzern (n=3), the University Children's Hospital Bern (n=1) and the University Children's Hospital Basel (n=1). The selection of the tumours for the study was based on the availability of a sufficient quantity of tumor tissue to perform RNA isolation. All diagnoses were confirmed by histological assessment of the tumor specimen obtained at surgery. An overview of the tumor characteristics is given in Supplemental Fig. 1.

Protein extraction from tumor samples. Tumor tissue was disrupted with a sterile disposable tissue grinder (Sage Products Inc.). Protein extracts were obtained using the PARIS Kit (Ambion) according to the manufacturer's instructions.

Isolation of RNA from tumor samples and RT-PCR. Tumor tissue was disrupted as described above and homogenised in guanidinium isothiocyanate-containing buffer. Total RNA was isolated using the RNeasy kit (Qiagen Inc.) according to the manufacturer's protocol. Total RNA (3 µg) from each tumor sample was converted into cDNA using the SuperScript™ First-Strand Synthesis System for PCR according to manufacturer's instructions (Invitrogen Life Technologies). mRNA expression of four target genes and 18S (internal control gene) was measured in tumor samples and cell lines by TaqMan® Assay-on-Demand™ Gene Expression products (Applied Biosystems). Normal human adrenal gland tissue (AG) was used as a reference. The following primers were used (gene – assay ID): PIK3R1 - Hs00236128_m1; PIK3CA - Hs00180679_m1; PIK3CB - Hs00178872_m1; PIK3CD - Hs00192399_m1; eukaryotic 18S rRNA - Hs99999901_s1. Three replicates were run for each sample in a 96-well format plate. Gene expression assays consisted of a FAM™ dye-labelled TaqMan® MGB probe and two PCR primers. The thermal cycling conditions consisted of an initial denaturation step at 95°C for 10 min and a 50-cycle countdown at 95°C for 15 s and 60°C for 1 min. Each sample was normalised on the basis of its 18S rRNA content. Relative mRNA expression levels were calculated using the comparative threshold cycle (CT) method (22).

Cell Culture. Human neuroblastoma cell lines were kindly provided by Dr Brodeur, Children's Hospital of Philadelphia. The cells were grown in RPMI (Life Technologies/Invitrogen) supplemented with 10% (v/v) fetal calf serum (FCS) and penicillin/streptomycin/L-glutamine and passaged every 3-5 days by trypsinization.

Stable Transfectants. SH-SY5Y and LA-N-1 cells were stably transfected with the murine ecotropic receptor (EcoR) using Lipofectamine (Invitrogen) according to the manufacturer's protocol. 72 hours post transfection, cells were diluted in medium containing G418 (0.8 mg/ml). In parallel, retroviral plasmid constructs encoding short hairpin RNA (shRNA) specifically targeting p110 α or p110 δ (23) were transiently transfected into packaging cells. The supernatant was diluted with 1 part RPMI containing G418 (final concentration: 0.8 mg/ml), as well as Polybrene (final concentration: 8µg/ml). The diluted supernatant was then added to cells stably expressing the EcoR. 24 hrs post infection, SH-SY5Y and LA-N-1 cells were split in medium containing puromycin (0.5 µg/ml). Single colonies were picked and

expanded in selective medium. Protein down-regulation was confirmed by Western blot analysis. All experiments were performed with two clones from each transfection.

Transient Transfection. Cells were transiently transfected using the Amaxa Nucleofector Device according to the optimised protocol provided for SH-SY5Y cells. The following constructs were used: pRS, pRS-PIK3CA, pRS-PIK3CD (23), pcDNA3 (Invitrogen) and pcDNA-S6K AK (9).

Cell Proliferation. Neuroblastoma cells were seeded in 96-well plates at a density of 7'500 cells/well and grown for 72 hrs in RPMI containing low (1%) or high (10%) serum. Alternatively, cells were treated with growth factors or inhibitors as indicated. Cell proliferation was analysed by the CellTiter 96[®] AQueous Cell Proliferation Assay (Promega) according to the manufacturer's instructions.

Apoptosis. Neuroblastoma cells were seeded in 96-well plates at a density of 20'000 cells/well. Basal caspase-3/7 activity was measured after 24 hrs using the Caspase-Glo[®] 3/7 Assay (Promega) according to the manufacturer's instructions.

Cell Cycle Distribution. Cell cycle distribution was analysed by means of propidium iodide (PI) staining and Fluorescence-activated cell sorter (FACS) analysis. Cells were seeded in a 6-well plate at a density of 6.5×10^5 cells and incubated in RPMI containing low (1%) or high (10%) serum for 24 hrs. Cells were collected using 0.5% trypsin and resuspended in cold PBS. One-tenth volume of 10x propidium iodide solution (500 µg/ml propidium iodide, 10mg/ml sodium citrate and 1% (v/v) Triton X-100) was added and cells were acquired in a flow cytometer within half an hour.

Growth Factor Stimulations. Cells were grown to confluency in a 6-well plate and starved overnight in RPMI containing 0.5% FCS. Cells were maintained in serum-free RPMI for 1 hour in the presence or absence of inhibitors as indicated and were then stimulated with the indicated growth factors for 10min. Cellular lysates were prepared as described below.

Western blotting. Cellular lysates were prepared as described (24) and normalised using a bicinchoninic acid (BCA) protein assay (Pierce). Cell lysates were separated by

sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE), transferred to a hydrophobic polyvinylidene difluoride (PVDF) membrane (Hybond-P; Amersham Biosciences) and immunoblotted with the indicated antibodies prior to chemiluminescent detection (ECL Western blotting detection reagents; Amersham Biosciences).

Statistical Analysis. Spearman's rank correlation and the Exact Wilcoxon rank-sum test were used for the analysis of PI3K gene expression in primary neuroblastoma samples. For experiments on cell lines, the statistical significance of differences between groups was assessed with ANOVA using the Bonferroni multiple comparison test, $p < 0.01$ were indicated with a double asterisk.

Results

Over-expression of PI3K isoforms in primary human neuroblastoma samples and cell lines. To gain insight into the specific functions of class I_A PI3K isoforms in neuroblastoma, we initially assessed the expression levels of the regulatory and catalytic subunits in two independent groups of tumor samples. In a panel of 19 primary neuroblastoma samples, the expression levels of the class I_A PI3K regulatory and catalytic subunits were analysed by quantitative RT-PCR (qRT-PCR) (Fig. 1A). Expression of the *PIK3R1* (encoding the regulatory subunit p85 α) and *PIK3CD* (encoding the catalytic subunit p110 δ) genes was found to be increased more than 2-fold in 10/19 neuroblastoma samples when compared to normal adrenal gland tissue (Fig. 1A, left panel). In contrast, mRNA expression of the catalytic p110 α and p110 β isoforms was not increased (Fig. 1A, left panel). In this panel of tumor samples, expression of p85 α and p110 δ was significantly correlated (Spearman's rank correlation, $p < 0.0001$), indicating that the p85 α /p110 δ heterodimer is over-expressed in neuroblastoma. Expression of p85 α and p110 δ was significantly higher in children under the age of one (median values: 2.48 for p85 α and 5.17 for p110 δ) than in patients older than one year of age (median values: 0.64 for p85 α and 0.95 for p110 δ) (Exact Wilcoxon rank-sum test, $p = 0.0121$ for p85 α ; $p = 0.0025$ for p110 δ). Furthermore, the expression of p85 α and p110 δ was found to be significantly lower in neuroblastoma samples with *MYCN* amplification (median values: 2.42 for p85 α and 4.63 for p110 δ) than without amplification (median values: 0.81 for p85 α and 0.75 for p110 δ) (Exact Wilcoxon rank-sum test, $p = 0.0339$ for p85 α ; $p = 0.0339$ for p110 δ). In contrast, no correlation was found between p85 α and p110 δ expression and tumor stage, 1p status or progression. Thus, p85 α and p110 δ expression was found to be increased in neuroblastoma samples from children under the age of one and with no *MYCN* amplification.

To investigate if *PIK3CD* mRNA levels are predictive of protein expression levels, Western blot analysis was performed on twelve of the patient samples. In 10/12 samples, mRNA levels correlated with protein expression (Fig 1A, right panel).

Reanalysis of cDNA microarray data of an independent panel of 68 primary neuroblastoma samples also revealed striking variations in the expression levels of the class I_A PI3K regulatory subunit p85 α and the catalytic subunit p110 δ . Expression of the p85 α and p110 δ subunits was significantly higher in samples from children under the age of one

compared to patients older than one year of age (Fig. 1B), confirming the results of the qRT-PCR analysis (Fig. 1A).

We next investigated the expression of PI3K isoforms in a set of 8 representative neuroblastoma cell lines to validate the findings obtained in tumor samples. In this panel of cell lines, p85 α was over-expressed in 5/8 samples, while the catalytic isoforms p110 α , p110 β and p110 δ showed increased expression in 4/8, 6/8 and 1/8 cell lines, respectively (Fig 1C, left panel). In line with the findings in patient samples, cell lines harbouring *MYC* amplification showed decreased levels of *PIK3CD* mRNA when compared to adrenal tissue (Fig 1C, left panel). As with the patient samples, mRNA levels were largely found to be predictive of protein levels (Fig 1C, right panel).

Insert Figure 1

The expression of PI3K isoforms was next investigated at the protein level in a panel of 8 neuroblastoma cell lines. All neuroblastoma cell lines included in this study expressed the p85 α , p110 α and p110 β isoforms, while the expression of p110 δ was more variable, being highest in SH-SY5Y cells (Fig. 2A). Together, these data show that the expression levels of PI3K isoforms are altered in neuroblastoma samples and cell lines at the mRNA and/or protein level, and that the expression of the catalytic p110 δ isoform is increased in neuroblastoma.

Insert Figure 2

Activation of PI3K/Akt signalling by polypeptide growth factors in neuroblastoma cell lines. Class I_A PI3Ks transduce signals from activated RTKs to downstream effectors, the most important of which is the Ser/Thr protein kinase Akt (12, 13). The activation of Akt by polypeptide growth factors was investigated in SH-SY5Y and LA-N-1 cells. Epidermal growth factor (EGF) and insulin-like growth factor-1 (IGF-1) most potently activated Akt in SH-SY5Y cells, while platelet-derived growth factor (PDGF) and IGF-1 induced the strongest response in LA-N-1 cells (Fig. 2B).

EGF and IGF-1 stimulated growth of SH-SY5Y (2 and 2.5-fold) and LA-N-1 (2 and 2.2-fold) cells, while PDGF was less potent at promoting a growth response (Fig. 2C). The pharmacological PI3K inhibitor LY294002 reduced basal growth of SH-SY5Y (66.5%

inhibition) and LA-N-1 (42.8% inhibition) cells. Treatment with the PI3K inhibitor also reduced EGF- and IGF-1-stimulated growth in SH-SY5Y (44.1% and 27.6% inhibition respectively) and LA-N-1 cells (Fig. 2C). However, LY294002 as a single agent did not significantly affect the extent of growth factor-stimulated cell growth in either SH-SY5Y or LA-N-1 cells (Fig. 2C). Recently, a similar observation was reported in neuroblastoma cell lines, where the combination of both LY294002 and the mTOR inhibitor rapamycin was required to inhibit IGF-1 induced proliferation (9). Thus, various growth factors, including EGF and IGF-1, stimulate growth of neuroblastoma cells via the PI3K/Akt pathway.

Impact of shRNA-mediated down-regulation of p110 α and p110 δ on neuroblastoma cell proliferation and apoptosis. To gain insight into the individual functions of class I_A PI3K isoforms in neuroblastoma cell responses, SH-SY5Y and LA-N-1 cells were stably transduced with short hairpin RNA (shRNA) constructs targeting p110 α (hereinafter p110 α^{low}) or p110 δ (hereinafter p110 δ^{low}). Specific down-regulation of target gene expression was verified by Western blot analysis (Fig. 3A). The growth of SH-SY5Y p110 δ^{low} cells was significantly reduced (53.1% and 44.1% inhibition) when the cells were cultivated in medium containing low (1%) serum, but not high (10%) serum (Fig. 3B). This effect was less pronounced in LA-N-1 cells (Fig. 3B), correlating with the differential expression of p110 δ in these cell lines. While an effect of p110 α down-regulation was also observed in SH-SY5Y cells (low serum: no inhibition or 21.3% inhibition; high serum: no inhibition or 21.2% inhibition), the effect was stronger in LA-N-1 cells (low serum: 22.1% and 66.4% inhibition; high serum: 11.7% and 43.4% inhibition).

To investigate whether PI3K targeting promoted apoptosis in neuroblastoma cells, caspase activity and cell cycle distribution were analysed in SH-SY5Y p110 α^{low} or p110 δ^{low} cells. A significant (2.2-fold) increase in caspase-3/7 activity was observed in SH-SY5Y p110 δ^{low} cells (Fig. 3C). In contrast, a comparable response was not observed in SH-SY5Y p110 α^{low} cells (Fig. 3C). Analysis of cell cycle distribution revealed a decrease in the S-phase in SH-SY5Y p110 α^{low} and p110 δ^{low} cells, both in low serum (61.8% decrease in both cases) and high serum (71.4% and 59.2% decrease). The increase in cell death under low serum conditions was higher in SH-SY5Y p110 δ^{low} cells (319.4% increase) than in SH-SY5Y p110 α^{low} cells (64.5% increase), confirming the results of the caspase assay (Fig. 3C). Together, these results demonstrate that the p110 δ isoform plays a major role in SH-SY5Y cell growth and survival under suboptimal culture conditions. In contrast, a comparable role

was not apparent for p110 α in these cells, although this isoform appeared to play a more important function in LA-N-1 cells, which express only very low levels of p110 δ .

In view of the increased apoptosis observed in SH-SY5Y p110 δ^{low} cells, we analysed the expression of pro- and anti-apoptotic Bcl-2 family proteins, which are key regulators of apoptosis. The levels of Bcl-2 and Bcl-X_L were elevated in SH-SY5Y cells grown in high serum, as compared to low serum conditions (Fig. 3D and 5B). When compared to control cells, SH-SY5Y p110 δ^{low} cells displayed reduced expression of the anti-apoptotic proteins Bcl-2 and Bcl-X_L (Fig. 3D and 5B). In contrast, the levels of Bax were unaffected (Fig. 3D). Thus, p110 δ appears to contribute to the control of the expression of anti-apoptotic Bcl-2 family proteins, which may impact on its function in neuroblastoma cell survival.

Insert Figure 3

Impact of shRNA-mediated down-regulation of p110 α and p110 δ on neuroblastoma cell responses to growth factors. We next investigated the involvement of class I_A PI3K isoforms in polypeptide growth factor signalling in neuroblastoma cells. The ability of EGF and IGF-1 to stimulate the growth of SH-SY5Y cells was significantly reduced in both SH-SY5Y p110 α^{low} and p110 δ^{low} cells (EGF: 6.4% and 40.3%, 23.4% and 16.2%, respectively; IGF-1: 27.5% and 41.5%, 42.1% and 49.1%, respectively) (Fig. 4A). In contrast, the ability of EGF and IGF-1 to stimulate the growth of LA-N-1 p110 α^{low} and p110 δ^{low} cells was not significantly impaired (Fig. 4A).

The impact of the shRNA constructs targeting p110 α and p110 δ on the activation of early signalling mediators of RTKs was then investigated in SH-SY5Y and LA-N-1 cells. Activation of Akt by EGF and IGF-1 was unaltered in SH-SY5Y and LA-N-1 cells (Fig. 4B and Supplemental Fig. 2). In contrast, activation of the mTOR/S6K pathway by EGF and IGF-1 was impaired in both SH-SY5Y p110 α^{low} and p110 δ^{low} cells, as assessed by phosphorylation of the S6 protein (Fig. 4B). While the impact of p110 α down-regulation on signal transduction was expected, the observation that decreased p110 δ expression leads to a comparable effect on its own was surprising. Activation of Erk1/2 by EGF and IGF-1 was unaffected by the PI3K shRNAs (data not shown). Thus, p110 δ plays an important role in activation of the mTOR/S6K pathway in SH-SY5Y cells, which correlates with its involvement in neuroblastoma cell growth. However, activation of Akt by growth factors is insensitive to down-regulation of a single PI3K isoform in these cells. This is not unexpected,

as previous studies have reported that PI3K isoforms from other classes contribute to Akt activation (24). In both LA-N-1 p110 α ^{low} and p110 δ ^{low} cells, basal activation of Akt and S6K was reduced (Supplemental Fig. 2). However, in LA-N-1 cells, phosphorylation of the S6 protein was hardly affected by down-regulation of p110 δ (Supplemental Fig. 2). While decreased p110 α expression led to a stronger inhibition of downstream signalling, no apparent effect on the proliferative response was observed, suggesting that other pathways may compensate for reduced signal transduction in this cell line (Fig. 4A and Supplemental Fig. 2).

Insert Figure 4

Constitutive activation of the S6K pathway abrogates the effect of p110 δ shRNA on SH-SY5Y cell growth. Our previous data had shown a marked effect of p110 δ down-regulation by shRNA on activation of the mTOR/S6K pathway in SH-SY5Y cells, contributing to cell growth. To confirm this model, SH-SY5Y p110 δ ^{low} cells were transiently transfected with an activated mutant of S6K1. Activated S6K promoted growth of SH-SY5Y cells and was able partially rescue the growth of SH-SY5Y p110 δ ^{low} cells (Fig. 5A). However, the induction of apoptosis induced by the p110 δ shRNA was only marginally impaired by S6K transfection, as assessed by cleavage of poly (ADP-ribose) polymerase (PARP) (Fig. 5B). Moreover, transient transfection of activated S6K did not restore the levels of Bcl-2 and Bcl-X_L in SH-SY5Y p110 δ ^{low} cells (Fig. 5B). Together, these results demonstrate that the PI3K p110 δ isoform controls neuroblastoma cell growth via the S6K pathway. In addition, it also appears to play a role in controlling the levels of Bcl-2 family proteins, which appears not to involve S6K or Akt.

Insert Figure 5

Rapamycin mimics the effects of p110 δ down-regulation. The data presented above highlighted the importance of signalling via the mTOR/S6K pathway in the regulation of neuroblastoma cell survival and the ability to respond to growth factors. To confirm these findings, SH-SY5Y and LA-N-1 cells were treated with rapamycin, an mTOR inhibitor, and cellular responses were investigated. As expected, phosphorylation of the S6 protein was abrogated in the presence of rapamycin, both in low (1%) and high (10%) serum conditions (Fig. 6A). Treatment of SH-SY5Y and LA-N-1 cells with rapamycin led to a dose-dependent

inhibition of basal cell proliferation (SH-SY5Y: 29.2% (20ng/ml) and 56.6% (100ng/ml) inhibition; LA-N-1: 37.3% (20ng/ml) and 61.8% (100ng/ml) inhibition) (Fig. 6B). Co-treatment of cells with rapamycin attenuated the proliferative response to EGF (SH-SY5Y: 34.7% (20ng/ml) and 55.8% (100ng/ml) inhibition; LA-N-1: 32.5% (20ng/ml) and 44.4% (100ng/ml) inhibition) and IGF-1 (SH-SY5Y: 32.5% (20ng/ml) and 53% (100ng/ml) inhibition; LA-N-1: 27.7% (20ng/ml) and 42.1% (100ng/ml) inhibition) (Fig. 6B). Furthermore, phosphorylation of the S6 protein was found to be absent upon stimulation with EGF or IGF-1 in cells pre-treated with rapamycin (Fig. 6C). These findings emphasise the importance of intact mTOR/S6K signalling in neuroblastoma cell survival.

Insert Figure 6

Discussion

In recent years, PI3K has emerged as a central controller of the cellular responses to a variety of growth factors and PI3K signalling is frequently deregulated by diverse mechanisms in human cancer (14, 16). PI3K has also been shown to play an important role in neuroblastoma biology. Therefore, targeting PI3K may represent an attractive approach to inhibit neuroblastoma proliferation *in vivo* (11, 17, 18, 25). However, the mechanisms contributing to the activation of PI3K signalling in neuroblastoma are still unclear, since loss of *PTEN* or *PIK3CA* mutations are uncommon in this paediatric malignancy (26-28). We show here for the first time that the class I_A PI3K isoform p110 δ plays a crucial role in neuroblastoma cell growth and survival and that the expression of p110 δ is increased at the mRNA and protein level in a subset of primary neuroblastoma samples and cell lines. In addition, our data reveal a selective expression of p85 α /p110 δ in neuroblastoma samples from children under the age of one. Our results also reveal a negative correlation between *PIK3CD* gene expression and *MYCN* amplification. Expression of *PIK3CD* was recently shown to be significantly lower in neuroblastoma samples with LOH at 1p36 (29). A recent study also described a correlation between decreased *PIK3CD* expression, 1p deletion and poor clinical outcome (30). LOH at 1p36 was associated with amplification of the *MYCN* oncogene (31). Reduced expression of *PIK3CD* in neuroblastoma samples may thus correlate with poor prognosis, due to its association with age at diagnosis (>1 year), LOH at 1p36 and/or *MYCN* amplification, since these events are prognostic markers of poor outcome in neuroblastoma (1, 2, 31, 32). N-Myc was shown to be able to replace IGF/PI3K signalling in medulloblastoma formation (33). Moreover, c-Myc expression had a negative impact on the activation of PI3K/Akt signalling (34). Thus, it is conceivable that *MYCN*-amplified neuroblastoma display decreased *PIK3CD* expression, either because of: (i) LOH at 1p36 (29); (ii) a direct negative effect of *MYCN* amplification on *PIK3CD* expression; or (iii) because they are less dependent on p85 α /p110 δ signalling. Collectively, these data indicate that the class I_A p110 δ isoform may play a role in the development of neuroblastoma in very young patients (<1 year of age), or in a subset of tumours which do not harbour LOH at 1p36 and/or *MYCN* amplification.

The expression of p110 δ was previously shown to be predominantly restricted to leukocytes in normal tissues (35). However, different human cancer cell lines were also shown to express this PI3K isoform, indicating that aberrant expression of p110 δ in tumours may contribute to the malignant properties of the cancer cells (24, 36). In support of this notion, the

ability of p110 δ to induce transformation of chicken fibroblasts was recently demonstrated (37). In breast cancer cell lines, a selective function of p110 δ in cell migration was also described (36). In acute myeloid leukemia, recent reports have shown that p110 δ plays a major role in activation of Akt by RTKs (FLT3), cell proliferation and chemoresistance (38, 39). We show here that the class I α PI3K isoforms p110 α and p110 δ do not have overlapping functions in neuroblastoma cell responses. Indeed, in SH-SY5Y cells which display increased *PIK3CA* and *PIK3CD* expression, p110 δ appeared to play a major role in controlling neuroblastoma cell growth and survival under limiting growth conditions. In contrast, in LA-N-1 cells with only very low p110 δ expression, down-regulation of p110 α by shRNA impaired cell growth and Akt activation. The impact of p110 δ down-regulation by shRNA on SH-SY5Y growth correlated with an impairment of the activation of the mTOR/S6K pathway. Surprisingly, Akt activation by EGF and IGF-1 was unaffected by p110 δ down-regulation, under conditions where the mTOR/S6K pathway was inhibited. Thus, activation of Akt and mTOR/S6K have different sensitivities to class I α PI3K down-regulation. It is conceivable that other PI3K isoforms may compensate for p110 α or p110 δ in growth factor-stimulated Akt activation (24). Transfection of an activated mutant of S6K was sufficient to partially rescue the growth defect of SH-SY5Y p110 δ^{low} cells under low serum conditions. However, p110 δ appeared to have an additional function in maintaining the levels of anti-apoptotic Bcl-2 family proteins in neuroblastoma cells, which did not involve S6K or Akt. The observation that the expression levels of anti-apoptotic Bcl-2 family proteins were higher in SH-SY5Y under high serum conditions, than in low serum, indicates that growth factors contribute to the regulation of the levels of Bcl-2 family proteins in these cells. Previous reports have documented a role for IGF-1, which is present in the FCS, in maintaining Bcl-2 (40) and Bcl-X $_L$ (41) expression levels. In view of the data presented here showing a role for p110 δ in IGF-1 signalling in neuroblastoma cells, it can be postulated that IGF-1R/p110 δ contributes to regulation of the expression of Bcl-2 family proteins. Since Akt and S6K were not involved in this pathway, the simplest explanation for these observations is that mTOR-mediated phosphorylation of 4E-BP1 controls translational activation of the expression of Bcl-2 and/or Bcl-X $_L$ in neuroblastoma cells, which is supported by previous findings in other systems (42). Down-regulation of p110 α by shRNA had a less pronounced impact on the growth of SH-SY5Y cells under low serum conditions, although activation of S6K was impaired. In view of the observation that p110 α down-regulation did not induce apoptosis in SH-SY5Y cells, in

contrast to p110 δ , it can be speculated that Bcl-2 family proteins are selectively controlled by the p110 δ isoform.

Together, our results demonstrate that p110 δ contributes to neuroblastoma cell growth and survival by regulating the activation of the mTOR/S6K pathway and the expression levels of anti-apoptotic Bcl-2 family proteins.

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Figure Legends

Fig. 1. Expression of class I_A PI3K genes in neuroblastoma patient samples and cell lines. *A*, TaqMan analysis of class I_A PI3K mRNA levels in neuroblastoma patient samples (n=19) and human adrenal gland (AG). *PIK3R1*: black bars, *PIK3CA*: light grey bars, *PIK3CB*: white bars, *PIK3CD*: dark grey bars (*left panel*). Western blot of p110 δ expression in patient samples (n=12) and AG compared to TaqMan data (*right panel*) *B*, Box plot visualising p85 α and p110 δ expression in an additional, independent group of 68 human neuroblastoma samples. *D*, Analysis of class I_A PI3K mRNA levels in human neuroblastoma cell lines (n=8) and AG. Colour code according to *A* (*left panel*). Western blot of p110 δ expression in cell lines (n=8) and AG compared to TaqMan data (*right panel*).

Fig. 2. PI3K class I_A isoform expression and growth factor-induced pathway activation in human neuroblastoma cell lines. *A*, Expression pattern of PI3K isoforms, Akt and the PI3K antagonist phosphatase and tensin homolog (PTEN) in human neuroblastoma cell lines. *B*, Growth factor-induced pathway activation in SH-SY5Y and LA-N-1 cells. *C*, Effect of LY294002 on growth factor-stimulated proliferation.

Fig. 3. Effect of class I_A PI3K isoform down-regulation on cell proliferation and cell death in human neuroblastoma cells. *A*, Western blot analysis of protein down-regulation in SH-SY5Y and LA-N-1 cells stably transfected with shRNA against p110 α (*PIK3CA*) or p110 δ (*PIK3CD*) or the control vector (pRS). *B*, Basal proliferation of SH-SY5Y or LA-N-1 cells in medium containing low (1%) or high (10%). *C*, Basal caspase-3/7 activity of SH-SY5Y clones in medium containing low (1%) or high (10%) serum (*left panel*). Cell cycle distribution of SH-SY5Y clones in medium containing low (1%) serum. Dead cells: black fraction; G2-phase: dark grey fraction; S-phase: white fraction; G0/G1-phase: light grey fraction (*right panel*) *D*, Western blot analysis of the expression levels of proteins involved in apoptosis in SH-SY5Y cells stably transfected with shRNA against p110 δ (*PIK3CD*) or the control vector (pRS) under low (1%) and high (10%) serum conditions.

Fig. 4. Proliferative response and pathway activation upon growth factor stimulation in cells expressing decreased levels of p110 α or p110 δ . *A*, Growth factor-induced proliferation of SH-SY5Y and LA-N-1 cells stably transfected with shRNA against p110 α (light grey bars)

or p110 δ (dark grey bars) or the control vector pRS (black bars). *B*, Growth factor-induced activation of the PI3K pathway in SH-SY5Y p110 α^{low} (PIK3CA) or p110 δ^{low} (PIK3CD) cells compared to control cells (pRS).

Fig. 5. Constitutively activated S6 kinase can partially rescue SH-SY5Y cells from cell death induced by p110 δ down-regulation. *A*, Proliferative response of SH-SY5Y p110 δ^{low} cells (PIK3CD) transiently transfected with constitutively activated S6 kinase 1 (S6K AK1) or the control vector (pcDNA3). *B*, Western blot analysis of the expression levels of proteins involved in apoptosis (Bcl2, Bcl-X_L, Bax) and PARP cleavage.

Fig. 6. Rapamycin mimics the effect of p110 δ down-regulation. *A*, Western blot analysis of S6 protein phosphorylation upon treatment of SH-SY5Y and LA-N-1 cells with rapamycin. *B*, Proliferation of SH-SY5Y and LA-N-1 cells in response to EGF and IGF-1 upon co-treatment with rapamycin (ng/ml where indicated). *C*, Western blot analysis of S6 protein phosphorylation in response to stimulation with EGF or IGF-1 upon pre-treatment with rapamycin.

Supplemental Fig. 1. Characteristics of human neuroblastoma patient samples as determined by histological assessment of the tumor specimen obtained at surgery. nd: not determined

Supplemental Fig. 2. Growth factor-induced activation of the PI3K pathway in LA-N-1 p110 α^{low} (PIK3CA) or p110 δ^{low} (PIK3CD) cells compared to control cells (pRS).

Figure 1

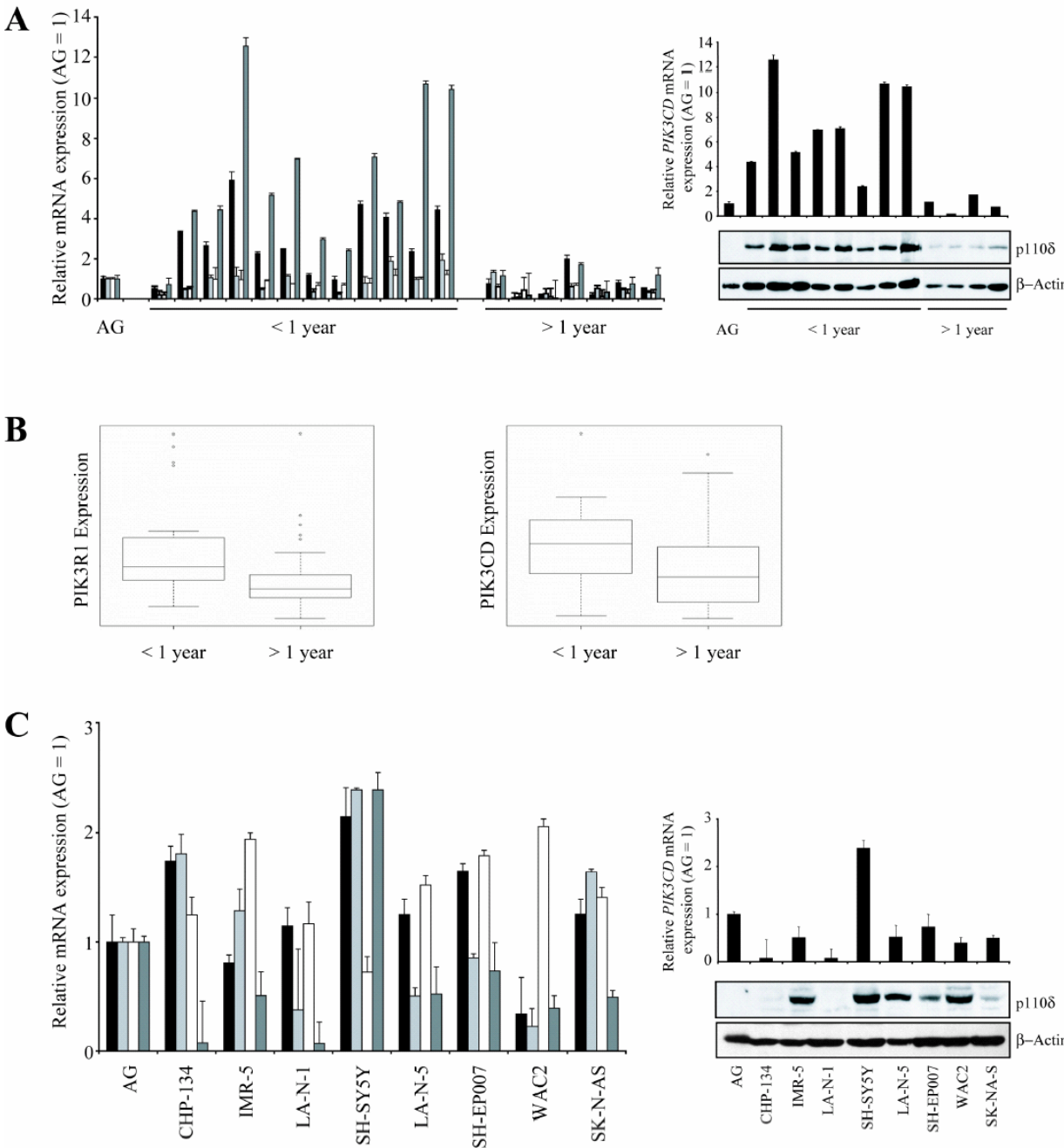


Figure 2

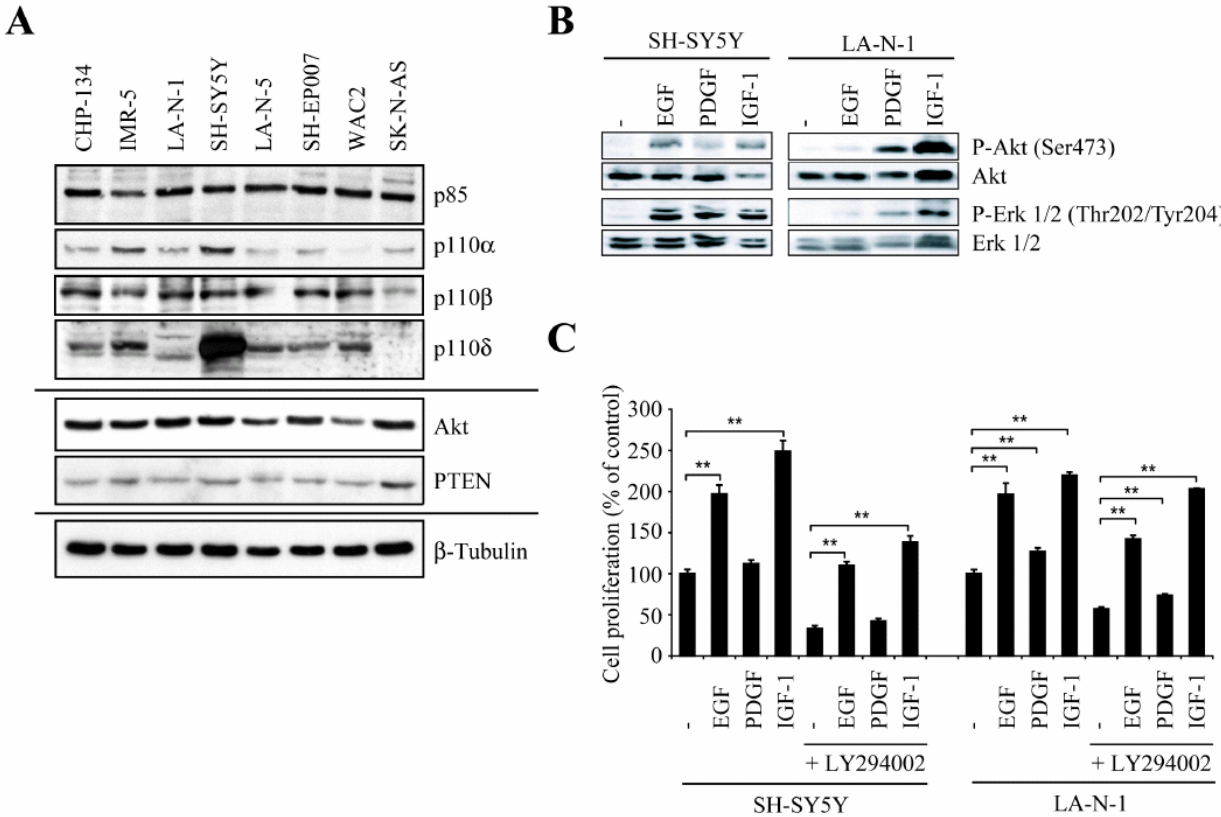


Figure 3

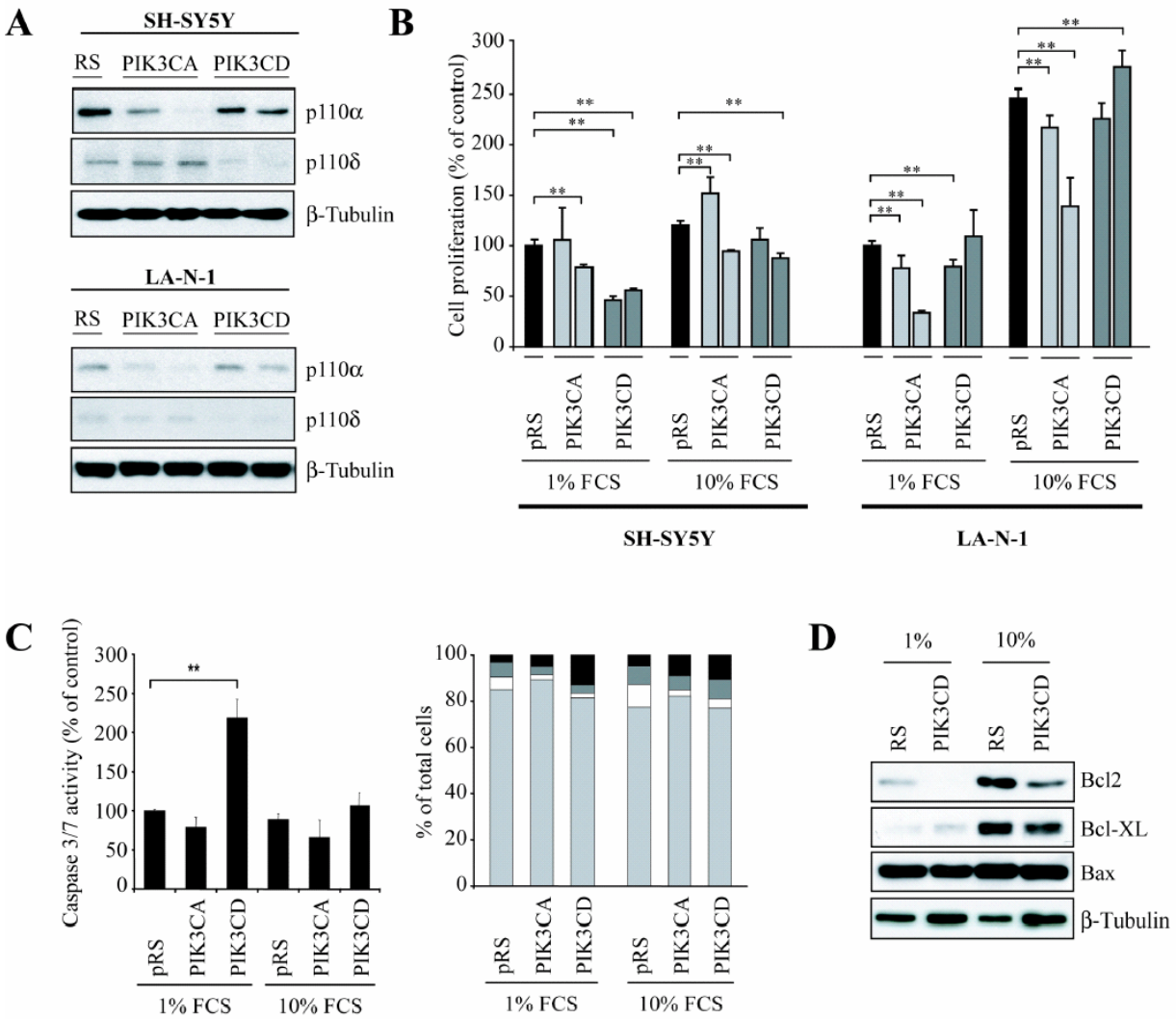


Figure 4

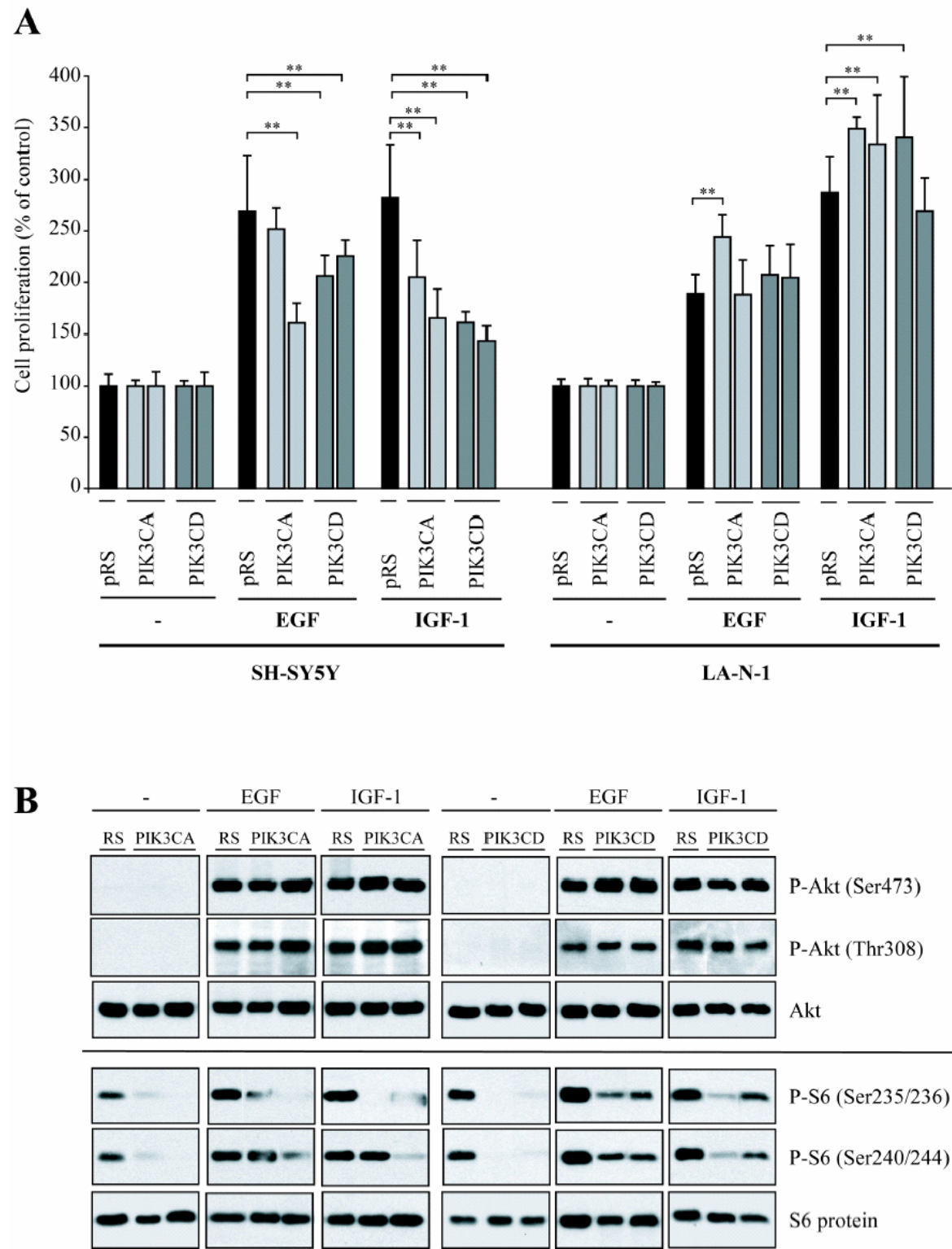


Figure 5

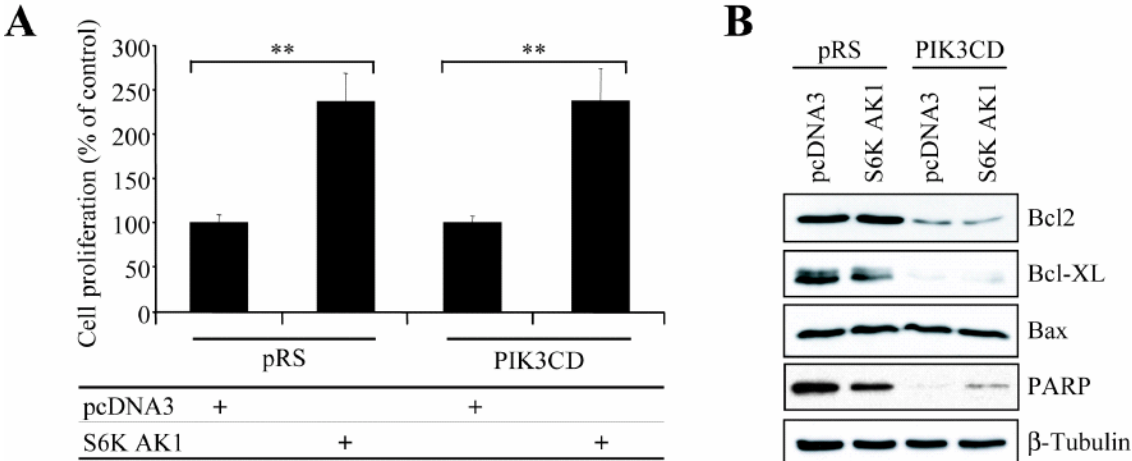
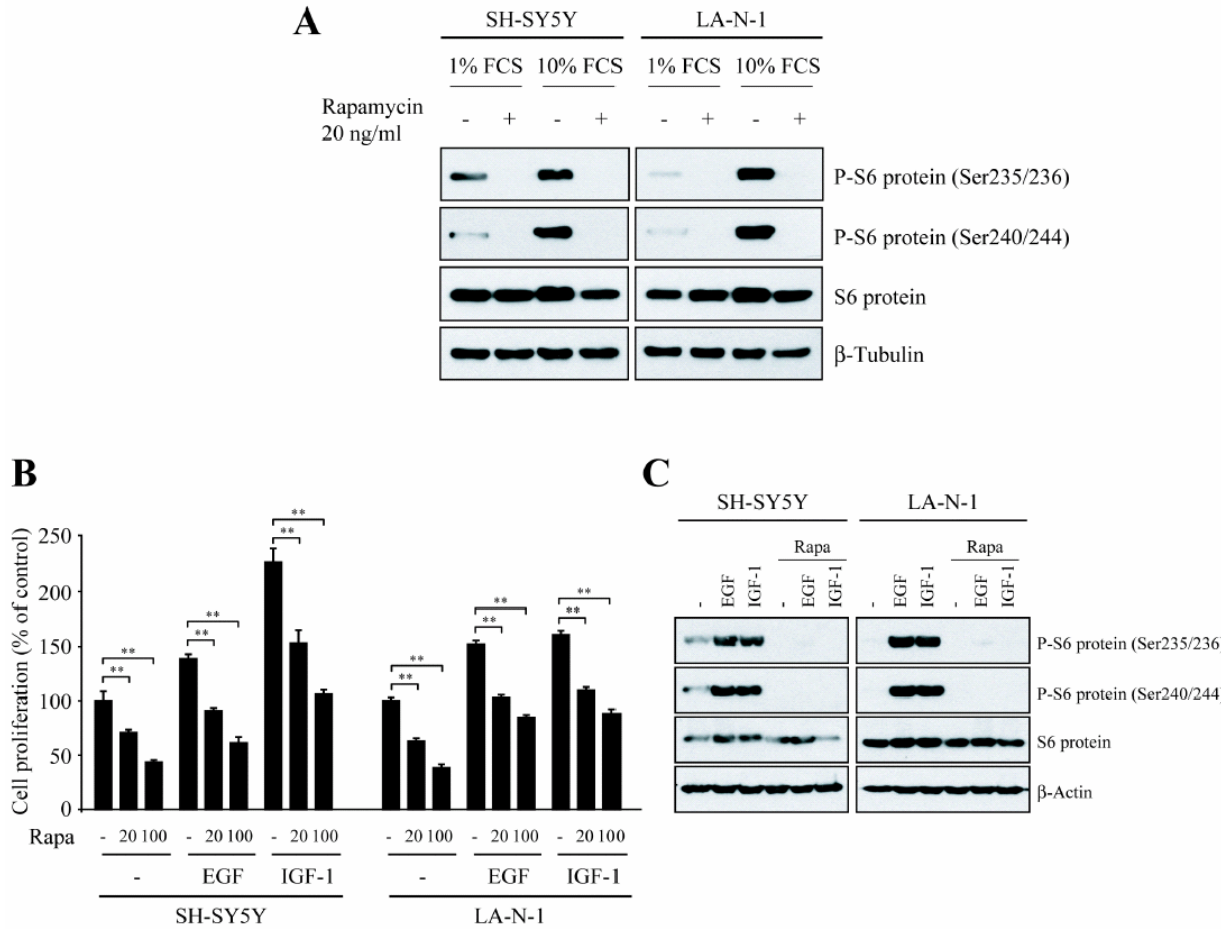


Figure 6



4. CONCLUSIONS AND PERSPECTIVES

A better understanding of the mechanisms underlying tumor formation has resulted in a new era of cancer treatment strategies using highly-specific inhibitors for gene targeted therapies. Extensive research aimed at identifying promising new molecular targets has placed RTK signaling into the front ranks. Several studies have proven a high efficacy of targeting the RTK system in cancer treatment and the use of novel small-molecule inhibitors lead to promising results and greatly reduced incidence rates of adverse side effects. Moreover, a trend towards combinatorial therapies, in which multiple signaling pathways are being targeted at the same time, is arising. Over the last years, great progress has been made in understanding the pathogenesis of AML revealing a number of promising targets, such as FLT3 and c-Kit. Despite the fact that clinical trials have corroborated the feasibility of using these newly developed agents in AML and have demonstrated acceptable tolerabilities in patients, they are not yet used as a standard treatment. Moreover, due to the heterogeneity of the disease, the inhibitors currently in clinical trials have only shown satisfactory results in certain subgroups of patients. Therefore, a number of other molecular targets remain yet to be discovered and this study was aimed at extending the current understanding of RTK signaling in human cancers, AML in particular, and the field of novel useful approaches.

The studies presented in this thesis on the IGF-IR/PI3K signaling system in AML blasts and cell lines highlighted the significant contribution of this network to cancer cell survival. We could show that IGF-I promotes growth and survival of AML blasts and that it activates intracellular signaling mediators including Akt and ERK. Furthermore, high expression levels of the IGF-IR were found in a panel of primary AML blasts and cell lines. Besides, we discovered that IGF-I was consistently secreted by the AML cells implying the presence of an autocrine signaling loop involving IGF-I and the IGF-IR. Previous studies had already described expression of the IGF-IR in human leukemias and over-expression of the IGF-IR was stated to harbingers transformation from MDS to AML as the IGF-IR appeared to have higher to lower expression rate in turn from AML to MDS to normal controls (Qi et al., 2006; Zumkeller & Burdach, 1999). Moreover, the expression of the IGF-IR negatively correlated with apoptosis suggesting a protective role for this receptor (Qi et al., 2006). Our finding of an autocrine IGF-I production and the involvement of the IGF-I/IGF-IR signaling system in AML cell growth and proliferation could be a more

relevant explanation for that survival advantage. Indeed we could show that blockage of the IGF-IR by different approaches suppressed AML cell growth at least in part by the induction of apoptosis.

In another study comparing the expression profiles of drug-resistant AML cells to drug-sensitive cells, an up-regulation of IGF-I could be associated with the resistance to the chemotherapeutical agent Ara-C (Abe et al., 2006). Consistently, IGF-I expression levels were found to be higher in patients at the refractory stage who received an Ara-C combined therapy, than in patients at diagnosis (Abe et al., 2006). It is a common finding that prolonged drug treatment can induce therapy resistance and that selected malignant cells can bypass the treatment efficacy by the activation of parallel signaling pathway. Indeed, sustained exposure of AML cells to tyrosine kinase inhibitors targeting FLT3 was shown to result in the activation of N-Ras and its signaling pathway (Piloto et al., 2007). Recently, another study described increased activation of the PI3K/Akt system upon treatment of AML patient blasts with the rapamycin derivative inhibitor everolimus (RAD001). Interestingly, the effect was explained by an IGF-I/IGF-IR autocrine signaling loop (Tamburini et al., 2007).

It is beyond question that we are still not familiar with all the sophisticated characteristics and reactions of cancer cells. However, current approaches targeting multiple signaling pathways definitively bear great potential in regard to treatment efficacy. In this notion, it was also our interest to investigate the potential of combining different targeting strategies. We could show that the use of NVP-AEW541 to block the IGF-IR kinase activity sensitized AML cells to chemotherapeutical agents and increased apoptosis. Besides, targeting the system further downstream by down-regulating or inhibiting the PI3K isoforms p110 β or p110 δ enhanced the action of etoposide or Ara-C. An important role of p110 δ in AML cell proliferation was already described before (Billottet et al., 2006; Sujobert et al., 2005). However, we could show for the first time that the class I PI3K p110 β was also widely expressed in the panel of AML cells analyzed and essentially contributed to cell growth.

While much attention has been paid to the understanding of the PI3K class I isoforms, little is known on the role of the other classes in regard to human cancer. Given the fact that also the class II isoforms were shown to integrate signals from growth factor receptors and to contribute to the generation of 3'-phosphoinositides, a potential role in cancer formation is certainly given (Arcaro et al., 2000). Indeed, recent studies have elucidated the role of PI3KC2 β in cytoskeletal

organization, cell migration and survival of human tumor cells (Katso et al., 2006; Maffucci et al., 2005). In this context, we conducted an extensive analysis of PI3KC2 β in a number of human tumors. We could show that PI3KC2 β was widely expressed in a panel of AML, glioblastoma multiforme, medulloblastoma, neuroblastoma, and small cell lung cancer cells. Over-expression of the mRNA as well as the protein was visible in certain subgroups, going in hand with previous studies that showed up-regulation of PI3KC2 β in a range of cancers including AML (Armstrong et al., 2002; Qian et al., 2002). By testing novel isoforms-specific inhibitors and siRNA to down-regulate PI3KC2 β we could show that also this PI3K isoform bears great potential as a therapeutic target. Different cancer cell lines were highly sensitive to PI3KC2 β inhibitors and strongly reduced cell proliferation rate in a dose-dependent manner. Besides, inhibiting PI3KC2 β sensitized AML and glioblastoma cells to chemotherapeutical agents. Taken together, we could describe an important role of PI3KC2 β for cell survival and chemo-sensitization in various tumors. Additionally, studying highly motile breast cancer cells underlined the finding that PI3KC2 β essentially contributes to cancer cell motility.

Studying expression patterns of RTK signaling molecules in AML cells lead to the interesting finding of highly variable mTOR levels in the panel of cells analyzed. A significant contribution of mTOR to AML cell growth and cell cycle control had been described before and constitutive activation of signaling pathways involving mTOR was shown to commonly occur in AML patients (Kubota et al., 2004; Martelli et al., 2006; Recher et al., 2005). We therefore aimed at gaining a better understanding of this rather unexpected finding and compared cells expressing high levels of mTOR (mTOR^{high} cells) to cells expressing low levels only (mTOR^{low} cells). By first comparing growth factor-induced pathway activation we could show that mTOR^{low} were not able to phosphorylate the mTOR downstream targets S6 protein and 4E-BP to the same extent as mTOR^{high} cells. However, activation/phosphorylation of the upstream molecule Akt was comparable. In a next step we compared the response to the mTOR inhibitor rapamycin in the two groups of cells. Surprisingly, no striking differences in regard to cell proliferation, induction of apoptosis and cell cycle could be detected. This finding raised the question of additional targets of rapamycin in AML which was further underlined by the result that cells expression high levels of mTOR indeed seemed to be more dependent on this protein. siRNA-induced down-regulation of mTOR namely significantly reduced cell proliferation in mTOR^{high} cells whereas

the growth rate of mTOR^{low} was not affected. A siRNA screen was therefore aimed at uncovering human kinases which modulate the sensitivity to rapamycin in AML. First results screening mTOR^{low} cells for proteins that had the strongest additive anti-proliferative effect brought the attention to certain RTKs such as the IGF-IR, FLT3 and the FGFR1, signal transducers such as SYK, ZAP70 and AKT1 to 3 as well as already well known oncogenes in leukemia like ABL1 and ABL2. Further experiments are now focused on validation of these candidates, on the one hand by the use of shRNA and on the other hand by the use of available inhibitors to specifically target the proteins. So far we could show that the candidates indeed play an important role in growth of the cancer cells and that targeting these kinases in combination with rapamycin bears great potential in regard to combinatorial cancer therapy. In a next step, mTOR^{high} cells will be screened using the same kinase library. The comparison with the mTOR^{low} cells will hopefully give further insight into the distinctness of the two groups and help elucidate the role of mTOR in AML cells.

In summary, the studies presented in this thesis underlined the significance of the RTK network in human cancer and yielded important findings which are relevant for the evaluation process of new molecular targets for AML.

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6. CURRICULUM VITAE

Kathrin T. Doepfner Curriculum Vitae

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Undergraduate Education

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1999–2004	Student of Biology at the University of Zurich, Zurich, Switzerland Major subjects: Zoology (Developmental Biology, Genetics, Ethology) Molecular Biology Minor subject: Computer Science

University

2000	1 st intermediate diploma
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2004	Master Degree in Zoology, dipl. zool.
2002–2003	Master Thesis Institute of Zoology, University of Zurich, Prof. Ernst Hafen <i>"Protein kinase Lk6 in Drosophila melanogaster: phosphorylation of eIF4E to control growth at the level of translation initiation"</i>
2004–2007	PhD Thesis University Children's Hospital Zurich, Division of Clinical Chemistry and Biochemistry, Dr. Alexandre Arcaro <i>"Targeting Receptor Tyrosine Kinase Signaling in Acute Myeloid Leukemia"</i>

Professional Education

1999 Assistant for Computer Applications/ Data Processing
SIS Swiss Financial Services Group AG, Zurich, Switzerland

2003–2004 Assistant for Student Courses

- Practical Course in Genetics for Biology Students, Institute of Zoology, University of Zurich (Prof. Andreas Dübendorfer)
- Practical Course in Developmental Biology for Medicine Students, Institute of Zoology, University of Zurich (Prof. Alex Hajnal)

2004 Research Assistant
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Societies

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Publication list

Original Research and Review articles

- 2005 Doepfner KT¹, Reiling JH¹, Hafen E, and Stocker H
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Diet-dependent effects of the Drosophila Mnk1/Mnk2 homolog Lk6 on growth via eIF4E
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- 2006 Guerreiro AS, Boller D, Doepfner KT, and Arcaro A
IGF-IR: Potential Role in Antitumor Agents
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- 2007 Doepfner KT, Boller D, De Laurentiis A, Guerreiro AS, Marinov M and Arcaro A: Recent
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Arcaro A
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neuroblastoma cells
Clinical Cancer Research (Manuscript in press)
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P, Robson A, Saghir N, Hayakawa M, Kaizawa H, Koizumi T, Ohishi T, Fattet S, Delattre
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Targeting PI3KC2β impairs proliferation and survival in acute leukemia, brain tumours
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Posters / Oral presentations

- 2005 Doepfner KT, Boller D, Arcaro A
Phosphatidylinositol-3 kinases as molecular targets for pediatric neuroblastoma and acute myeloid leukemia
 USGEB-SSN-SSBP Meeting 2005, ETH Zurich (Poster)
- Doepfner KT, Spertini O, Arcaro A
Phosphatidylinositol-3 kinases as molecular targets for acute myeloid leukemia
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 4th Day of Clinical Research, University Hospital Zurich (Poster)
- Doepfner KT, Spertini O, Arcaro A
Phosphatidylinositol-3 kinases as molecular targets for acute myeloid leukemia
 Journée des Jeunes Chercheurs en Pédiatrie, University of Bern (Oral Presentation)
- 2006 Doepfner KT, Spertini O, Arcaro A
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 Poster presentation 2006, University Children's Hospital Zurich (Poster)
- Doepfner KT, Spertini O, Arcaro A
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 5th Day of Clinical Research, University Hospital Zurich (Poster)
- Doepfner KT, Spertini O, Arcaro A
Autocrine insulin-like growth factor signaling promotes growth and survival of human acute myeloid leukemia cells via the Phosphatidylinositol-3 kinase pathway
 4th Swiss Apoptosis Meeting, University of Bern (Oral Presentation and Poster)
- Doepfner KT, Spertini O, Arcaro A
Autocrine insulin-like growth factor signaling promotes growth and survival of human acute myeloid leukemia cells via the Phosphatidylinositol-3 kinase pathway
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- Doepfner KT, Spertini O, Arcaro A
Autocrine insulin-like growth factor signaling promotes growth and survival of human acute myeloid leukemia cells via the Phosphatidylinositol-3 kinase pathway
 Targeting the Kinome, Congress Center Basel (Poster)
- 2007 Doepfner KT, Spertini O, Arcaro A
mTOR Expression Levels and Rapamycin Sensitivity in Acute Myeloid Leukemia Cells
 6th Day of Clinical Research, University Hospital Zurich (Poster)

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mTOR Expression Levels and Rapamycin Sensitivity in Acute Myeloid Leukemia Cells

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BACR – Cell Signalling and Novel Cancer Therapeutics, London (Poster)

Boller D, Schramm A, Doepfner KT, Shalaby T, Von Bueren OA, Eggert A, Grotzer MA, Arcaro A

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